

From: Bowman, Amy
Sent: Tuesday, June 28, 2005 1:39 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/735,991

Hello,
I need SEQ ID NO: 5 in application 10/735,991 searched.
Thank you,
Amy Bowman
AU 1635
REM 2C31
571-272-0755

1014NA

Beverly shears

STAFF USE ONLY

Searcher: _____
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Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

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CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC
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Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CGN

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 08:57:44 ; Search time 645 Seconds
(without alignments)
9306.384 Million cell updates/sec

Title: US-10-735-991-5

Sequence: 1 atgaactcgtgcgagcgcgg99.....ttctgcgcgtgtctgagtcga 1014

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014	100.0	1014	12	ADQ94493
2	1011	99.7	1011	12	ADQ94489
3	1010.8	99.7	1014	6	ABK47595
4	1010.8	99.7	1014	12	ADQ29763
5	1009.2	99.5	2530	13	ADQ89177
6	1009.2	99.5	2581	2	AAZ00034
7	1006.2	99.2	1728	10	ADT70549
8	986.8	97.3	1014	6	ABK73406
9	869.2	85.7	1011	12	ADQ29057
10	868.4	85.6	1172	12	ADQ94491
11	556.6	54.9	565	5	AAK68630
12	472.2	46.6	585	9	ACH39042
13	418.2	41.2	1092	5	AAK07950
14	418.2	41.2	1092	11	ADJ96477
15	416.6	41.1	5665	10	ABK24430
16	415	40.9	1092	3	AAK64108
17	415	40.9	1092	4	AAK59997
18	415	40.9	1092	4	AAK08865
19	415	40.9	1092	4	AAH73502
20	415	40.9	1092	5	AAK08268

21	415	40.9	1092	6	AAK26313	AAK26313 Human G-P
22	415	40.9	1092	8	ABA00881	ABA00881 Somatost
23	415	40.9	1092	11	ADL96541	ADL96541 Human mlt
24	415	40.9	1092	13	ADK09774	ADK09774 Human the
25	415	40.9	1163	6	ABK41643	ABK41643 Human G-P
26	415	40.9	1163	6	AAH51105	AAH51105 Human ncp
27	415	40.9	1188	4	ABK70338	ABK70338 DNA encod
28	415	40.9	1188	4	ABK70338	ABK70338 DNA encod
29	415	40.9	1352	6	ABK53077	ABK53077 Human DNA
30	415	40.9	1510	4	AAK46219	AAK46219 Human DNA
31	415	40.9	1510	8	ACA89669	ACA89669 DNA encod
32	415	40.9	1510	8	ACA73679	ACA73679 Human sec
33	415	40.9	1510	8	ACA05994	ACA05994 Human sec
34	415	40.9	1510	8	ACA68828	ACA68828 DNA encod
35	415	40.9	1510	8	ACF20403	ACF20403 Human sec
36	415	40.9	1510	8	ACF19789	ACF19789 Human sec
37	415	40.9	1510	8	ACD22077	ACD22077 Human sec
38	415	40.9	1510	8	ACD25345	ACD25345 Human sec
39	415	40.9	1510	8	ACF00394	ACF00394 Human sec
40	415	40.9	1510	8	ACA72451	ACA72451 Novel hum
41	415	40.9	1510	8	ACD04975	ACD04975 Novel hum
42	415	40.9	1510	8	ACD18436	ACD18436 Human sec
43	415	40.9	1510	8	ACD08443	ACD08443 Human sec
44	415	40.9	1510	8	ACA88877	ACA88877 Novel hum
45	415	40.9	1510	8	ACA70319	ACA70319 Human sec

ALIGNMENTS

RESULT 1
ADQ94493 standard; cDNA; 1014 BP.
ID ADQ94493
XX
AC ADQ94493:
XX
DT 23-SEP-2004 (first entry)
XX
DE Human G-protein coupled receptor sequence 115 cDNA.
XX
XX anorectic; immunomodulator; gene therapy; body weight;
KW mammalian sequence 115; obesity; cachexia; G protein coupled receptor;
KW sequence 115; human; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT CDS 1..1014
FT FT /product= "Human G-protein coupled receptor sequence 115"
XX
XX US2004121395-A1.
XX
XX 24-JUN-2004.
XX
XX 15-DEC-2003; 2003US-00735991.
XX
XX 23-DEC-2002; 2002US-0436375P.
XX
XX (GOOD/) GOODNOW R A.
XX (MARK/) MARK D F.
XX (MART/) MARTIN M L.
XX (ROST/) ROSTINSKI J A.
XX
XX Goodnow RA, Mark DF, Martin ML, Rosinski JA,
XX .MPI; 2004-468185/44.
XX P-PSDB; ADQ94494.
XX
XX Identifying compounds, useful for modulating body weight and for treating
XX obesity and cachexia, comprises contacting a test compound with a
XX mammalian sequence 115.

PS Claim 36; SEQ ID NO 5; 28bp; English.

XX The invention describes a method of identifying compounds useful for
 CC modulating body weight, comprising contacting a test compound with a
 CC mammalian sequence 115. The method comprises: contacting a test compound
 CC with a mammalian sequence 115; determining whether the test compound
 CC binds to the mammalian sequence 115; and identifying a compound that
 CC binds to the mammalian sequence 115 as a compound useful for modulating
 CC body weight. Also described are: a pharmaceutical formulation or
 CC composition, for modulating body weight, comprising a compound that
 CC modulates the activity of a mammalian sequence 115, mixed with a
 CC pharmaceutical carrier; a package comprising the pharmaceutical
 CC formulation and instructions for administering the pharmaceutical
 CC formulation for modulating body weight; preparing a pharmaceutical
 CC composition useful for modulating body weight; treating obesity and
 CC cachexia; and an antibody that recognizes an isolated polypeptide
 CC comprising a sequence of 1014 or 337 amino acids (SEQ ID NOS: 5 or 6).
 CC The method is useful for identifying compounds useful for modulating body
 CC weight. The formulation or composition and methods are useful for
 CC treating obesity and cachexia. This sequence encodes human G protein
 CC coupled receptor sequence 115.

SO Sequence 1014 BP; 152 A; 363 C; 301 G; 198 T; 0 U; 0 Other;

Query Match 100.0%; Score 1014; DB 12; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 1.2e-172;
 Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ATGAACCTGTGGAGCGGGGCTTGGGCTTACTGTGGGACAGATGGGCTTCGCTG 60
DB 1 ATGAACCTGTGGAGCGGGGCTTGGGCTTACTGTGGGACAGATGGGCTTCGCTG 60
OY 61 CTGTCCAAACGCGGTGCTGCTGTGCTGTGACAGCGGAGCATCCGCGCAGACG 120
DB 61 CTGTCCAAACGCGGTGCTGCTGTGCTGTGACAGCGGAGCATCCGCGCAGACG 120
OY 121 CCGGCGCTCTTACCTTGAACTCACTGTGCGGAACTGTGTGCACTGTGTCAATG 180
DB 121 CCGGCGCTCTTACCTTGAACTCACTGTGCGGAACTGTGTGCACTGTGTCAATG 180
OY 181 CCGCTCAAGCTGGCGGCTGTGGCGGAGGAGCGCGGCGGAGCGCGCTGTGCGG 240
DB 181 CCGCTCAAGCTGGCGGCTGTGGCGGAGGAGCGCGGCGGAGCGCGCTGTGCGG 240
OY 241 CTGGCTGCTTCTCTGACACCTTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 CTGGCTGCTTCTCTGACACCTTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 300
OY 301 AGCATCGACCGCTGAGTGGCTGTGCTTCCGCTGAGCTACCGGAGCAAGATGCGCTC 360
DB 301 AGCATCGACCGCTGAGTGGCTGTGCTTCCGCTGAGCTACCGGAGCAAGATGCGCTC 360
OY 361 CCGGACCGGCGCTCATTGATGAGCTTACAGCTGTGAGCGGCTCACTTCCGAGCGCC 420
DB 361 CCGGACCGGCGCTCATTGATGAGCTTACAGCTGTGAGCGGCTCACTTCCGAGCGCC 420
OY 421 GCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
OY 481 CCGGCGGCGGAGCGAGCGGCTTGGCGCTTCACTGCGGCTTCAAGCTCTTCAGC 540
DB 481 CCGGCGGCGGAGCGAGCGGCTTGGCGCTTCACTGCGGCTTCAAGCTCTTCAGC 540
OY 541 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
OY 601 TTCCATTGCAAGCGATGACGATGATGACGATGACGATGACGATGACGATGACGATG 660
DB 601 TTCCATTGCAAGCGATGACGATGATGACGATGACGATGACGATGACGATGACGATG 660
OY 661 CACCCAGTGTGCGGAAAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
  
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DB 661 CACCCAGTGTGCGGAAAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
OY 721 AAGAATGACGACCTTCAATAGGACCTTCTGTGTGCTTGGCGGCTATGTATGATCAC 780
DB 721 AAGAATGACGACCTTCAATAGGACCTTCTGTGTGCTTGGCGGCTATGTATGATCAC 780
OY 781 AGCTAGTGAAGCTCTTCTTCCACGAGTGGCCCATGCTGCTCCCATGAGGGGCTGTCCAA 840
DB 781 AGCTAGTGAAGCTCTTCTTCCACGAGTGGCCCATGCTGCTCCCATGAGGGGCTGTCCAA 840
OY 841 TGTGTGCGTACAGAGCGGATCGATCCGACCCCTTGTGTGACTCTTACTGACACAG 900
DB 841 TGTGTGCGTACAGAGCGGATCGATCCGACCCCTTGTGTGACTCTTACTGACACAG 900
OY 901 TACCGAAAAGCTGCAAGAGATTTGAAACAGGCTCTGACAGAGCGTCCATCACTCC 960
DB 901 TACCGAAAAGCTGCAAGAGATTTGAAACAGGCTCTGACAGAGCGTCCATCACTCC 960
OY 961 TCTGGCTTCAAGGCACTCTTCAAGCCAGACATTCTGCGGTGTGTAGTGA 1014
DB 961 TCTGGCTTCAAGGCACTCTTCAAGCCAGACATTCTGCGGTGTGTAGTGA 1014
  
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RESULT 2
AD094489 AD094489 standard; cDNA; 1011 BP.
XX
AC AD094489;
DT 23-SEP-2004 (first entry)
XX
DE Mouse G-protein coupled receptor sequence 115 cDNA.
XX
KW anorectic; immunomodulator; gene therapy; body weight;
KW mammalian sequence 115; obesity; cachexia; G protein coupled receptor;
KW sequence 115; mouse; gene; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..1011
FT CDS /tag=a
FT /product= "Mouse G-protein coupled receptor sequence 115"
XX
PN US2004121395-A1.
PD 24-JUN-2004.
XX
PP 15-DEC-2003; 2003US-00735991.
XX
PR 23-DEC-2002; 2002US-0436375P.
XX
PA (GOOD/) GOODNOW R. A.
PA (MARK/) MARK D F.
PA (MART/) MARTIN M L.
PA (ROSI/) ROSINSKI J A.
XX
PI Goodnow RA, Mark DF, Martin ML, Rosinski JA.
XX
DR WPI; 2004-468185/44.
DR P-PSDB; AD094490.
XX
PT Identifying compounds, useful for modulating body weight and for treating
PT obesity and cachexia, comprises contacting a test compound with a
PT mammalian sequence 115.
XX
PS Example 3; SEQ ID NO 1; 28bp; English.
XX
CC The invention describes a method of identifying compounds useful for
CC modulating body weight, comprising contacting a test compound with a
CC mammalian sequence 115. The method comprises: contacting a test compound
CC with a mammalian sequence 115; determining whether the test compound
  
```

QY	1	ATGAACTGTGTGGAGAGCGGGGCTCTGCGGGGCTTATGTGTGGGACGATGGGCGTTCGTG	60
Db	1	ATGAACCTGTGTGGAGAGCGGGGCTCTGCGGGGCTTATGTGTGGGACGATGGGCGTTCGTG	60
QY	61	CTGTCCAAAGCGCTGTGTGCTGTGCTGCCTGCTGACAGGCGGGACATCCGCGCCGAGGGG	120
Db	61	CTGTCCAAAGCGCTGTGTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120
QY	61	CTGTCCAAAGCGCTGTGTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120
Db	61	CTGTCCAAAGCGCTGTGTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120
QY	121	CCGGGCGCTCTTACACCTGTAACCTGACGTCGCGGAACTCTGTGTGACACGCTGTGCAACATG	180
Db	121	CCGGGCGCTCTTACACCTGTAACCTGACGTCGCGGAACTCTGTGTGACACGCTGTGCAACATG	180
QY	121	CCGGGCGCTCTTACACCTGTAACCTGACGTCGCGGAACTCTGTGTGACACGCTGTGCAACATG	180
Db	121	CCGGGCGCTCTTACACCTGTAACCTGACGTCGCGGAACTCTGTGTGACACGCTGTGCAACATG	180
QY	181	CCGCTCAAGCTGTGGCGGCGGTGTGTGGGACGCGGACGCGCGGCGACCGCTGTGCGCG	240
Db	181	CCGCTCAAGCTGTGGCGGCGGTGTGTGGGACGCGGACGCGCGGCGACCGCTGTGCGCG	240
QY	241	CTGGCTGTGCTTCTCTGACACCTTCTCTGTGGGTGCACTGCTGTGACATGTGCTGTGACATGTG	300
Db	241	CTGGCTGTGCTTCTCTGACACCTTCTCTGTGGGTGCACTGCTGTGACATGTGCTGTGACATGTG	300
QY	301	AGCATCGACGCTGTGGGTGGCGGTGTGCTTCCGCTGAGCTACCGGGCCAAAGATGCGGCTTC	360
Db	301	AGCATCGACGCTGTGGGTGGCGGTGTGCTTCCGCTGAGCTACCGGGCCAAAGATGCGGCTTC	360
QY	361	CGCGACGCGGGGCTCATGTGTGGCTTACACGTGTGGCTGACACGCGCTCACTTTCGACGCGCT	420
Db	361	CGCGACGCGGGGCTCATGTGTGGCTTACACGTGTGGCTGACACGCGCTCACTTTCGACGCGCT	420
QY	421	GGCGTGGCGCTGTCTGTGTGTGGCTGGGCTTCCACACGATGATACGCTGTGACACGCTGTGACAC	480
Db	421	GGCGTGGCGCTGTCTGTGTGTGGCTGGGCTTCCACACGATGATACGCTGTGACACGCTGTGACAC	480
QY	481	CGGGGCGGACGAGCGGCTGTGGCTTCCGCTTTCACCTGCGGCTTCCACGCTCTCAGC	540
Db	481	CGGGGCGGACGAGCGGCTGTGGCTTCCGCTTTCACCTGCGGCTTCCACGCTCTCAGC	540
QY	541	TTTCTGTCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	600
Db	541	TTTCTGTCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	600
QY	601	TTTCATTTGCAAGCGCATGACGATGATACACATGACGATGATGATGATGATGATGATGATGATG	660
Db	601	TTTCATTTGCAAGCGCATGACGATGATACACATGACGATGATGATGATGATGATGATGATGATG	660
QY	661	CACCCCAATGTGTGGGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	720
Db	661	CACCCCAATGTGTGGGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	720
QY	721	AAGAAAGATACACACTTATATAGGACCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
Db	721	AAGAAAGATACACACTTATATAGGACCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780

CC to) diseases

New G protein-coupled receptor AXOR49, useful for diagnosis and treatment of e.g. infections and cancer.

Claim 2; Page 27; 34pp; English.

The present invention relates to a new polypeptide encoded by a polynucleotide comprising a fully defined sequence of 1014 base pairs, as given in the specification. The polypeptide of the invention comprises a sequence at least 95% identical to a fully defined sequence of 337 amino acids as given in the specification, or a fragment or variant. The polypeptide, a putative G protein-coupled receptor designated AXOR49, and the nucleic acid that encodes it are useful for treating a very wide range of diseases, e.g. infections (bacterial, viral, fungal or protozoal), especially human immune deficiency virus-1 or -2), pain, cancer, diabetes, Parkinson's diseases, heart failure and allergy. The molecules of the invention can also be used to diagnose (susceptibility to) diseases (including detecting mutations or measuring mRNA or protein

CC Levels) associated with inappropriate activity or levels of AXOR49, to
CC screen for (ant)agonists, potential therapeutic agents and in vaccines.
CC The present nucleic acid sequence encodes the human G protein coupled
CC receptor AXOR49 protein of the invention
XX
SQ Sequence 1014 BP; 151 A; 364 C; 301 G; 198 T; 0 U; 0 Other;

Query Match 99.7%; Score 1010.8; DB 6; Length 1014;
Best Local Similarity 99.8%; Pred. No. 4,4e-172;
Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAACCTGTTGGAGACGGGGCTTGGCGGCTACTGGTGGGACAGATGGGCTTCGCTG 60
DB 1 ATGAACCTGTTGGAGACGGGGCTTGGCGGCTACTGGTGGGACAGATGGGCTTCGCTG 60
QY CTGTCCAAAGCGGCTGGTGGTCTGTCTGTCTGTGACAGCGGAGCATCCGCGCAGAGCG 120
DB 61 CTGTCCAAAGCGGCTGGTGGTCTGTCTGTCTGTGACAGCGGAGCATCCGCGCAGAGCG 120
QY 121 CCGGCGCTCTTCAACCTTGAACCTTGCAGCTGGGAGAACTGTGTGCAACCGTGTCAACATG 180
DB 121 CCGGCGCTCTTCAACCTTGAACCTTGCAGCTGGGAGAACTGTGTGCAACCGTGTCAACATG 180
QY 181 CCGCTCACGCTGGCGCGGCTGTGGCGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 181 CCGCTCACGCTGGCGCGGCTGTGGCGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 241 CTGGGCTCTCTCTCTGACACCTTCTGTGGTCCAACTGCATGTCTGACATGTGGCGGCTC 300
DB 241 CTGGGCTCTCTCTCTGACACCTTCTGTGGTCCAACTGCATGTCTGACATGTGGCGGCTC 300
QY 301 AGCATGACCGCTGGTGGTGGCGGCTGTCTGTGTGAGCTAACCGGAGCAAGATGGGCTC 360
DB 301 AGCATGACCGCTGGTGGTGGCGGCTGTCTGTGTGAGCTAACCGGAGCAAGATGGGCTC 360
QY 361 CGGAGCGCGGCTGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 361 CGGAGCGCGGCTGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 421 GCGCTGCGGCTGTCTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB 421 GCGCTGCGGCTGTCTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 481 CGGCGGCGGAGCGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 481 CGGCGGCGGAGCGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 541 TTCTGTGCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 541 TTCTGTGCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 601 TTTCATTGCAAGCGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 TTTCATTGCAAGCGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 CACCCAGTGTGCGGAGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 661 CACCCAGTGTGCGGAGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
QY 721 AAGAAGATGAGACCTTCTATAGGAGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 721 AAGAAGATGAGACCTTCTATAGGAGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
QY 781 AGGCTAGTGGAGCTCTTCTCAAGGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 840
DB 781 AGGCTAGTGGAGCTCTTCTCAAGGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 840
QY 841 TGCTTGGGTATACAGAGCGGAGATTCGAGACCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 TGCTTGGGTATACAGAGCGGAGATTCGAGACCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 TACGCAAAAGCTGAGAGAGATTTGTGACAGGCTCTGTGACAGACGCTCATCATCTCC 960
DB 901 TACGCAAAAGCTGAGAGAGATTTGTGACAGGCTCTGTGACAGACGCTCATCATCTCC 960

DB 901 TACGCAAAAGCTGAGAGAGATTTGTGACAGGCTCTGTGACAGACGCTCATCATCTCC 960
QY 961 TCTGGGCTTCAAGCGGAGCTTCTCAAGCGAAGATTTCTGGGTGTGTAGTGA 1014
DB 961 TCTGGGCTTCAAGCGGAGCTTCTCAAGCGAAGATTTCTGGGTGTGTAGTGA 1014
RESULT 4
AD029763
ID AD029763 standard; cDNA; 7512 BP.
XX
AC AD029763;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human novel GPCR GPR26 polynucleotide, SEQ ID NO:865.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; urens disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; vasotropic; antihistaminic; antianemic;
KW CNS; central nervous system; respiratory; antidiabetic; antidiabetic;
KW virology; hepatotropic; antibacterial; antianemic; antidiabetic;
KW dermatological; antihistaminic; antihistaminic; anorectic;
KW immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN NO200404000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003MO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
PI Galitanaris GA, Bergmann JB, Gragerov A, Hohmann J, Li F;
PI Medisen L, McIlwain KL, Pavlova MN, Vasiliadis D, Zeng H;
XX WPI; 2004-390329/36.
DR P-PSDB; ADO29055.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
PS
PS Claim 13; SEQ ID NO 865; 542pp; English.
XX
CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridize to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of

CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
 CC nucleic acid of the invention. Note: The full sequence data for this
 CC patent did not form part of the printed specification; those sequences
 CC not shown were obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences.
 CC XX
 SQ Sequence 7512 BP; 1779 A; 1828 C; 1976 G; 1929 T; 0 U; 0 Other;

Query Match 99.7%; Score 1010.8; DB 12; Length 7512;
 Best Local Similarity 99.8%; Pred. No. 4.6e-172;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAACCTGCGGAGCGGCGCTTGGGCGGCTATGCTGCGGCGGCGCTTCCGCTG 60
 DB 53 ATGAACCTGCGGAGCGGCGCTTGGGCGGCTATGCTGCGGCGGCGCTTCCGCTG 112
 QY 61 CTGTCCAAAGCGGCGGCGCTTGGGCGGCTATGCTGCGGCGGCGGCGGCGGCGGCGG 120
 DB 113 CTGTCCAAAGCGGCGGCGCTTGGGCGGCTATGCTGCGGCGGCGGCGGCGGCGGCGG 172
 QY 121 CGGCGCGCTTTCACCTTGAACCTTCAAGCGGAGAACCTGCTGTCACCGGTGTCACATG 180
 DB 173 CGGCGCGCTTTCACCTTGAACCTTCAAGCGGAGAACCTGCTGTCACCGGTGTCACATG 232
 QY 181 CGGCTACCGCTGCGGCGGCGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 DB 233 CGGCTACCGCTGCGGCGGCGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 292
 QY 241 CTGGGCTGCTTCCGCGGCGGCGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 DB 293 CTGGGCTGCTTCCGCGGCGGCGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 352
 QY 301 AGCATGACCGCTGCGGCGGCGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
 DB 353 AGCATGACCGCTGCGGCGGCGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 412
 QY 361 CGGAGCGGCGGCGCTCATGTGCGCTTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 DB 413 CGGAGCGGCGGCGCTCATGTGCGCTTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 472
 QY 421 GCGCTGCGGCGGCGCTCATGTGCGCTTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
 DB 473 GCGCTGCGGCGGCGCTCATGTGCGCTTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 532
 QY 481 CGGCGGCGGCGGCGGCGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
 DB 533 CGGCGGCGGCGGCGGCGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 592
 QY 541 TTCTGCTGCTTCTTGTGCTGCTTGTGTCAGGTAAGTCAAGGTGTCAGGTAAGTCAAG 600
 DB 593 TTCTGCTGCTTCTTGTGCTGCTTGTGTCAGGTAAGTCAAGGTGTCAGGTAAGTCAAG 652
 QY 601 TTCTGCTGCTTCTTGTGCTGCTTGTGTCAGGTAAGTCAAGGTGTCAGGTAAGTCAAG 660
 DB 653 TTCTGCTGCTTCTTGTGCTGCTTGTGTCAGGTAAGTCAAGGTGTCAGGTAAGTCAAG 712
 QY 661 CACCCAGTGTGCGGAGACGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 DB 713 CACCCAGTGTGCGGAGACGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 772
 QY 721 AAGAAGATCAAGCACTTCAATAGGAGACTTCTTGTGTGCTTGTGCGGCGGCGGTAAGTCA 780

DB 773 AAGAAGATCAAGCACTTCAATAGGAGACTTCTTGTGTGCTTGTGCGGCGGCGGTAAGTCA 832
 QY 781 AGGCTAGTGAAGCTCTTCTCAAGGTCGCGGCTCCCACTGGGGGGTGTCTCCAG 840
 DB 833 AGGCTAGTGAAGCTCTTCTCAAGGTCGCGGCTCCCACTGGGGGGTGTCTCCAG 892
 QY 841 TGCTGGCGTACAGAGAGCGCGCATCCGACCCCTTGTGTACTTCTTACTGCGACACG 900
 DB 893 TGCTGGCGTACAGAGAGCGCGCATCCGACCCCTTGTGTACTTCTTACTGCGACACG 952
 QY 901 TACCGAAAGCTGCAAGAGATTTGAAACAGGCTCCTGACAGAGAGCGCTCCATCCATCC 960
 DB 953 TACCGAAAGCTGCAAGAGATTTGAAACAGGCTCCTGACAGAGAGCGCTCCATCCATCC 1012
 QY 961 TCTGGCTCAAGGCGGCGCTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1014
 DB 1013 TCTGGCTCAAGGCGGCGCTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1066

RESULT 5
 ADQ89177
 ID ADQ89177 standard; cDNA; 2530 BP.
 XX AC ADQ89177;
 XX DT 21-OCT-2004 (first entry)
 XX DE Human urological disorder related protein 2882 encoding cDNA SEQ.129.
 XX KW urological disorder; uropathic; cytostatic; urinary incontinence;
 XX KM benign prostatic hyperplasia; human; gene; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 186..1199
 XX FT /*tag= a
 XX FT /product= "urological disorder related protein 2882"
 XX PN NO2004065576-A2.
 XX PD 05-AUG-2004.
 XX XP 14-JAN-2004; 2004MO-US000750.
 XX PF 15-JAN-2003; 2003US-0440318P.
 XX PR 04-FEB-2003; 2003US-044783P.
 XX PR 27-MAR-2003; 2003US-0457901P.
 XX PR 08-MAY-2003; 2003US-0468775P.
 XX PR 19-MAY-2003; 2003US-0471614P.
 XX PR 16-JUN-2003; 2003US-0478742P.
 XX PR 18-JUL-2003; 2003US-0488529P.
 XX PR 30-JUL-2003; 2003US-0491156P.
 XX PR 02-SEP-2003; 2003US-0495954P.
 XX PR 26-SEP-2003; 2003US-0506332P.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Karichet V, Silos-Santiago I, Eliasoof SD;
 XX DR WPI; 2004-562167/54.
 XX DR P-FSDB; ADQ89178.
 XX XX
 XX XX Use of polypeptides related to urological disorders, e.g. 44390, 54181,
 XX XX 211 or for identifying a compound capable of treating a urological
 XX XX disorder or identifying and treating a subject having a urological
 XX XX disorder.
 XX PS Claim 1; SEQ ID NO 129; 542pp; English.
 XX XX
 XX CC The present invention describes the use of polypeptides related to
 CC urological disorders for identifying a compound capable of treating a

Db	301	AGCATGACCGCTGGGTGGCCGTGGTCTTCCCGCTGAGCTACCGGGCCAAAGATGCGCTC	360
Qy	361	CGGAGCGCGCGCTCATGGTGGCTTACAAGTGGCTGACGCGCTCACCTTCCAGCGCC	420
Db	361	CGGAGCGCGCGCTCATGGTGGCTTACAAGTGGCTGACGCGCTCACCTTCCAGCGCC	420
Qy	421	GCGCTGGCTGTCTGCTGGGTCTCCACAGCTGTATAGGCTGGTGCAGCGTGTGAGC	480
Db	421	GCGCTGGCTGTCTGCTGGGTCTCCACAGCTGTATAGGCTGGTGCAGCGTGTGAGC	480
Qy	481	CGGCGGCGCAGACGAGGCGCTGGGCTTCCGCGCTTCACTGGCGCTTCCAGCTCTGAG	540
Db	481	CGGCGGCGGCGAGCGAGCGCTTGGCGCTTCCAGCTGGCGCTTCCAGCTCTGAG	540
Qy	541	TTCTGTGCTCTCTTGGTGGTGTCTGTGTCAGAGTCAAGTGTCTCAAGTGTGGCCGC	600
Db	541	TTCTGTGCTCTCTTGGTGGTGTCTGTGTCAGAGTCAAGTGTCTCAAGTGTGGCCGC	600
Qy	601	TTTCATTGGCAAGCGCATCGACGTGATCACATATGCAGAGCGCTGTGTGTGGAACTTG	660
Db	601	TTTCATTGGCAAGCGCATCGACGTGATCACATATGCAGAGCGCTGTGTGTGGAACTTG	660
Qy	661	CACCCCAAGTGTGGGGAAGCTGTCTGGAGGAGGAGGAGGCGGAGCGCAGCGACACC	720
Db	661	CACCCCAAGTGTGGGGAAGCTGTCTGGAGGAGGAGGAGGCGGAGCGCAGCGACACC	720
Qy	721	AAGAAGATCAGACCTTTCATTAAGGACCTTCTTGTGTCTTGGCGCTATGTATACCC	780
Db	721	AAGAAGATCAGACCTTTCATTAAGGACCTTCTTGTGTCTTGGCGCTATGTATACCC	780
Qy	781	AGGCTAATGAGACTCTTCTCCACGCGTCCCATGGCTCCACTGGGGGGTGTCTCCAG	840
Db	781	AGGCTAATGAGACTCTTCTCCACGCGTCCCATGGCTCCACTGGGGGGTGTCTCCAG	840
Qy	841	TGCTTGGCGTACAGCAAGGCGGATCCGACCCCTTGTGTCTCTTAATGCGCACACAG	900
Db	841	TGCTTGGCGTACAGCAAGGCGGATCCGACCCCTTGTGTCTCTTAATGCGCACACAG	900
Qy	901	TACCGCAAAAGCTGCAAGAGATTTGAAACAGGCTCTGACAGAGCTCCATCACTCC	960
Db	901	TACCGCAAAAGCTGCAAGAGATTTGAAACAGGCTCTGACAGAGCTCCATCACTCC	960
Qy	961	TCTGGCTCTCAGGCGCATCTTCCACAGCCAGAAATTCTGGCGGTGTGAG	1011
Db	961	TCTGGCTCTCAGGCGCATCTTCCACAGCCAGAAATTCTGGCGGTGTGAG	1011
RESULT 8			
AB573406			
XX	ID	AB573406 standard; cDNA; 1014 BP.	
XX	AC	AB573406;	
XX	DT	04-DEC-2002 (first entry)	
XX	DE	cDNA encoding human GPCR GPR26.	
XX	XX	Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; myocardiial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; gene; ss.	
OS	XX	Homo sapiens.	
XX	PN	W0200268600-A2.	
XX	PD	06-SEP-2002.	
XX	PF	26-FEB-2002; 2002WO-US005625.	

Query Match	97.3%	Score 386.8	DB 6	Length 1014	
Beet Local Similarity	98.3%	Pred. No. 8.7e-168			
Matches 997	Conservative 0	Mismatches 17	Indels 0	Gaps 0	
XX 26-FEB-2001; 2001US-0271913P.					
XX (AREN-) ARENA PHARM INC.					
XX PA Liew CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;					
XX P1 Lin I, Ortuno D;					
XX MPI; 2002-706980/76.					
XX P-PSDB; ABG95179.					
XX New human G-protein coupled receptor (GPCR), useful for screening agonist					
XX PT or inverse agonist compounds for treating diseases associated with GPCR.					
XX PS Example 1; Page 198-199; 201pp; English.					
XX The present invention relates to transmembrane receptors, particularly					
XX CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-					
XX CC endogenous) versions of the GPCRs, and the polynucleotide sequences					
XX CC encoding them. The GPCRs are useful for screening agonist or inverse					
XX CC agonist compounds for treating diseases associated with GPCR. Diseases					
XX CC that can be treated with such compounds include allergies, hypertension,					
XX CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic					
XX CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),					
XX CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,					
XX CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present					
XX CC sequence encodes an endogenous human GPCR					
XX Sequence 1014 BP; 153 A; 364 C; 298 G; 199 T; 0 U; 0 Other;					
1 ATGAACCTGTTGGAGCGCGGCGCTGGCGGGGCTACTGTTGTTGGGAGAGATGGGCTCTGCTG 60					
1 ATGAACCTGTTGGAGCGCGGCGCTGGCGGGGCTACTGTTGTTGGGAGAGATGGGCTCTGCTG 60					
61 CTGTTCACAGCGCTGTGTGCTCTGTCTGTCTGTGCACAGCGCGGACATCGCGCCGACGCG 120					
61 CTGTTCACAGCGCTGTGTGCTCTGTCTGTCTGTGCACAGCGCGGACATCGCGCCGACGCG 120					
121 CCGGCGCTCTTCACTGACCTGACCTGACCTGCGGGAACCTGTGTGTGACCTGTGTCAACATG 180					
121 CCGGCGCTCTTCACTGACCTGACCTGACCTGCGGGAACCTGTGTGTGACCTGTGTCAACATG 180					
181 CCGCTCAAGCGTGGCGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240					
181 CCGCTCAAGCGTGGCGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240					
241 CTGGCTGCTCTTCTGTGACCTCTTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 300					
241 CTGGCTGCTCTTCTGTGACCTCTTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 300					
301 AGCATTCAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360					
301 AGCATTCAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360					
361 CCGCAGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420					
361 CCGCAGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420					
421 GCGCTGCGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480					
421 GCGCTGCGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480					
481 CCGCGCGCGAGAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540					
481 CCGCGCGCGAGAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540					
541 TTCCGCTCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600					
541 TTCCGCTCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600					

QY 601 TTCCATTGCAAGCGCATCGAGTATGATCACCATGAGACGCGTGGTGGTGGAGCTG 660
 DB 601 TTCCATTGCAAGCGCATCGAGTATGATCACCATGAGACGCGTGGTGGTGGAGCTG 660
 QY 661 CACCCAGTGTGCGGGAACGCTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 DB 661 CACCCAGTGTGCGGGAACGCTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 QY 721 AAGAGATGAGCAGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 DB 721 AAGAGATGAGCAGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 QY 781 AGGCTATGAGGAGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
 DB 781 AGGCTATGAGGAGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
 QY 841 TGCTTGGCTGACAGCAGGCGGATCCGAGCCCTTGTGTACTCTTACTGCGACAGCAG 900
 DB 841 TGCTTGGCTGACAGCAGGCGGATCCGAGCCCTTGTGTACTCTTACTGCGACAGCAG 900
 QY 901 TACCGCAAAAGCTGCAAGAGATTCTGAACAGGCTCTGCAAGAGGCTCCATCCATCC 960
 DB 901 TACCGCAAAAGCTGCAAGAGATTCTGAACAGGCTCTGCAAGAGGCTCCATCCATCC 960
 QY 961 TCTGGCTTCAAGGCGGCTCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1014
 DB 961 TCTGGCTTCAAGGCGGCTCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1014

RESULT 9

ADO29057 standard; cDNA, 1011 BP.

ADO29057;

29-JUL-2004 (first entry)

Mouse novel GPCR GPR26 polynucleotide, SEQ ID NO:156.

G protein-coupled receptor; GPCR; drug screening; diagnosis;
 transgenic mouse; neurological disorder; adrenal gland disorder;
 colon disorder; intestinal disorder; cardiovascular disorder;
 muscular disorder; blood disorder; immune disorder; bone disorder;
 joint disorder; metabolic disorder; nutritive disorder; cancer;
 kidney disorder; liver disorder; lung disorder; breast disorder;
 ovary disorder; uterus disorder; prostate disorder; testis disorder;
 skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 thymus disorder; thyroid disorder; antiparkinsonian; antiemetic;
 cytoskeletal; antiinflammatory; vasodilator; antidiabetic;
 CNS; central nervous system; respiratory; antidiabetic; antidiabetic;
 vitamin; hepatotropic; antibacterial; antianemic; antiseborrheic;
 dermatological; antitumor; antihypertensive; anorectic;
 immunosuppressive; nephroretic; gene therapy; GPCR modulator; mouse;
 murine; gene; ss.

Mus musculus.

W02004040000-A2.

13-MAY-2004.

09-SEP-2003; 2003MO-US028226.

09-SEP-2002; 2002US-0409303P.

09-APR-2003; 2003US-0461329P.

(PRIM-) PRIMAL INC.

Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,

Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;

WPI; 2004-390329/36.

P-PSDB; ADO29056.

XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 pectoris, Parkinson's disease.

Claim 13; SEQ ID NO 156; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors
 (GPCRs) and nucleic acids encoding them. The invention also relates to
 sequences at least 90% identical to the GPCR proteins and nucleic acids
 of the invention; methods of treating, preventing or diagnosing diseases
 associated with GPCRs of the invention; methods of screening for
 compounds useful in the treatment of GPCR-related diseases; a transgenic
 mouse comprising a GPCR gene of the invention; a mouse comprising a
 mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 from the transgenic mice; kits comprising several mice, each of which has
 a mutation in a different GPCR gene of the invention; and kits comprising
 probes which hybridize to GPCR polynucleotides of the invention. The
 invention further discloses variants of the GPCR polypeptides and vectors
 comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 be used in the diagnosis, treatment or prevention of a wide variety of
 diseases including neurological disorders (e.g., Alzheimer's disease,
 depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 disorders of the adrenal gland; disorders of the colon or intestine
 (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 myocardial infarction); muscular disorders; blood disorders (e.g.,
 anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 diseases); and disorders of the kidney, liver, lung, breast, ovary,
 uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 thyroid (e.g., cancer). The present sequence represents a GPCR-encoding
 nucleic acid of the invention. Note: The full sequence data for this
 CC patent did not form part of the printed specification; those sequences
 CC not shown were obtained in electronic format directly from WPI at
 ftp.wpi.int/pub/published_pct_sequences.

SQ Sequence 1011 BP; 165 A; 347 C; 282 G; 217 T; 0 U; 0 Other;

Query Match 85.7%; Score 869.2; DB 12; Length 1011;
 Best Local Similarity 91.3%; Pred. No. 1e-146;
 Matches 922; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1 ATGAATCTGCTGGAGACCGGCGCTGGGCGGCTACTGCTGGGACGATGGCGCTGCTG 60
 DB 1 ATGAATCTGCTGGAGACCGGCGCTGGGCGGCTACTGCTGGGACGATGGCGCTGCTG 60
 QY 61 CTGTCCAGCGCGTGTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 DB 61 CTGTCCAGCGCGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 QY 121 CCGGCGCTCTTCAACCTGAACTCACGTGGGGAACCTGTGTGCAACCGTGTCAACATG 180
 DB 121 CCGGCGCTCTTCAACCTGAACTCACGTGGGGAACCTGTGTGCAACCGTGTCAACATG 180
 QY 181 CCGCTACAGCTGGCGCGGCTGTGTGCGGACGCGGCGGCGGCGGCGGCGGCGGCGG 240
 DB 181 CCGCTACAGCTGGCGCGGCTGTGTGCGGACGCGGCGGCGGCGGCGGCGGCGGCGG 240
 QY 241 CTGGCTGCTCTTCTGACACCTTCTGAGCGCACTCCATGCTGCAATGGCGGCGGCTC 300
 DB 241 CTGGCTGCTCTTCTGACACCTTCTGAGCGCACTCCATGCTGCAATGGCGGCGGCTC 300
 QY 301 AGCATGACCGCTGGTGGCGGTGATCTTCCGCTGAGTACCGGCGCAAGATGCGGCTC 360
 DB 301 AGCATGACCGCTGGTGGCGGTGATCTTCCGCTGAGTACCGGCGCAAGATGCGGCTC 360
 QY 361 CGCGACGCGGCGCTCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 DB 361 CGAGATGCGGCGCTTCAATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

XX ACH39042;
 XX 13-OCT-2003 (first entry)
 DT
 XX Human foetal brain cDNA #409.
 DE
 XX Human; ss; sequencing by hybridisation; SHH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX Homo sapiens.
 OS
 XX US2003073623-A1.
 PN
 XX 17-APR-2003.
 PD
 XX 30-JUL-2001; 2001US-00918995.
 XX
 XX 30-JUL-2001; 2001US-00918995.
 PF
 XX 30-JUL-2001; 2001US-00918995.
 PR
 XX (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.
 DR
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX
 XX Claim 1; SEQ ID NO 26254; 44pp; English.
 PS
 XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SHH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030073623
 CC
 XX Sequence 585 BP; 118 A; 182 C; 161 G; 118 T; 0 U; 6 Other;
 SQ
 XX
 XX Query Match 46.6%; Score 472.2; DB 9; Length 585;
 XX Best Local Similarity 99.4%; Pred. No. 1.4e-75;
 XX Matches 474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 707 GACAGGAGCCACCAAGAAATGACGACCTTCA TAGGACCTTCTGTGTGCTTGCGCG 766
 DB 229 GACAGGAGCCACCAAGAAATGACGACCTTCA TAGGACCTTCTGTGTGCTTGCGCG 288
 QY 767 CCTATGATACCAAGGCTAGTGAAGCTCTTCA CAGGAGCCATCGGCTCCCACTGGG 826
 DB 289 CTTATGTGATCACCAGGCTAGTGAAGCTCTTCA CAGGAGCCATCGGCTCCCACTGGG 348
 QY 827 GGGTGTGTCGACAGTGTGCGGTACAGCAAGGCGGCATCCGACCCCTTGTGTACTCT 886
 DB 349 GGGTGTGTCGACAGTGTGCGGTACAGCAAGGCGGCATCCGACCCCTTGTGTACTCTCT 408
 QY 887 TACTGGACACCAAGTACCGGAAAGCTGCAAGAGATTCTGMA CAGGCTCCGCAAGAC 946
 DB 409 TACTGGACACCAAGTACCGGAAAGCTGCAAGAGATTCTGMA CAGGCTCCGCAAGAC 468
 QY 947 GCTCCATCCACTCTCTGAGCTCAGCAGGAGCTCTCAGACGCGAGACATTTCTGCGG 1003
 DB 469 GCTCCATCCACTCTCTGAGCTCAGCAGGAGCTCTCAGACGCGAGACATTTCTGCGG 525

RESULT 13
 AAS07950
 ID AAS07950 standard; cDNA; 1092 BP.
 AC AAS07950;
 XX
 XX 23-OCT-2001 (first entry)
 DT
 XX Human cDNA encoding G-protein coupled receptor, hrup23.
 DE
 XX Human; G-protein coupled receptor; GPCR; hrup23; agonist;
 KW inverse agonist; lung cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1092
 FT /*tag= a
 FT /product= "hrup23"
 FT
 XX
 XX W0200136471-A2.
 PN
 XX
 PD 25-MAY-2001.
 XX
 XX 16-NOV-2000; 2000WO-US031509.
 PF
 XX
 XX 17-NOV-1999; 99US-0166088P.
 PR 17-NOV-1999; 99US-0166099P.
 PR 17-NOV-1999; 99US-0166369P.
 PR 23-DEC-1999; 99US-0171900P.
 PR 23-DEC-1999; 99US-0171901P.
 PR 23-DEC-1999; 99US-0171902P.
 PR 11-FEB-2000; 2000US-0181749P.
 PR 14-MAR-2000; 2000US-0189258P.
 PR 14-MAR-2000; 2000US-0189259P.
 PR 10-APR-2000; 2000US-0195898P.
 PR 10-APR-2000; 2000US-0195899P.
 PR 10-APR-2000; 2000US-0196078P.
 PR 28-APR-2000; 2000US-0200419P.
 PR 12-MAY-2000; 2000US-0203630P.
 PR 12-JUN-2000; 2000US-0210741P.
 PR 12-JUN-2000; 2000US-0210982P.
 PR 21-AUG-2000; 2000US-0226760P.
 PR 26-SEP-2000; 2000US-0235418P.
 PR 26-SEP-2000; 2000US-0235779P.
 PR 20-OCT-2000; 2000US-0242343P.
 PR 20-OCT-2000; 2000US-0242343P.
 PR 24-OCT-2000; 2000US-0243019P.
 XX
 XX (AREN-) ARENA PHARM INC.
 PA
 XX Chen R, Dang HT, Lowitz KP;
 PI

XX WPI; 2001-355616/37.
 DR P-PSDB; AAU04377.
 XX Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents.
 XX Example 1; Page 117; 160pp; English.
 XX The sequence encodes a human G-protein coupled receptor (GPCR), hRUP23.
 CC The endogenous and non-endogenous, constitutively activated versions of
 CC human G-protein coupled receptors (GPCR), are useful for direct
 CC identification of candidate compounds as receptor agonists, inverse
 CC agonists or partial agonists having applicability as therapeutic agents
 CC for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous
 CC version of human GPCRs are also utilized in research settings and in
 CC vitro and in vivo system, incorporating GPCRs can be utilized to
 CC elucidate and understand the roles these receptors play in the human
 CC condition, both normal and diseased

XX Sequence 1092 BP; 151 A; 397 C; 340 G; 204 T; 0 U; 0 Other;

Query Match 41.2%; Score 418.2; DB 5; Length 1092;
 Best Local Similarity 64.5%; Pred. No. 6.8e-66;
 Matches 624; Conservative 0; Mismatches 343; Indels 0; Gaps 0;

QY 1 ATGAATCTGTGGAGCGCGGCGCTGAGCTACTGTGGGACAGATGGGCTCTGCTG 60
 DB 1 ATGGGCCCCGGGAGGGGCTGCTGCGGGCTCTCTGGTGAATGTAATGCGCTGG 60
 QY 61 CTGTTCACAGCGCGTGTGTCTCTCTGCTGTGCAACAGCGGAGCAATCGCGCCAGCG 120
 DB 61 CTATTCACAGCGAGTGTGTCTCTGTGTGCGCTCAACAGCGCTGAGCTCGGACGACC 120
 QY 121 CCGGCGCTCTTCACTCCGTAACCTCACGTGCGGGAACCTGTGTGACAGCTGTCAATG 180
 DB 121 TCAGGCGCTCTCTGTGTAATCTGTGTGCGGCACTGTGCGGCGCTGTGAGACATG 180
 QY 181 CCGCTCAAGCTGTGGCGGCGTGTGTGCGGAGCGGAGCGGCGGAGCGCGCTGTGCGCG 240
 DB 181 CCGCTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 QY 241 CTGGCTGCTCTCTGTGACACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 DB 241 GTCAATGAGCTCTGTGACACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 QY 301 AGCATCAACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
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 QY 361 CCGGACGCGGCGCTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 DB 361 CCGCTATGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 QY 421 GCGCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 DB 421 GCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
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 DB 481 CCGGCGGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
 QY 541 TTCTGTGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
 DB 541 TTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
 QY 601 TTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 DB 601 AGCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 QY 661 CACCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720

DB 661 CACCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
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 DB 721 AAGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
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 DB 781 AGGCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
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 DB 841 TGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
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 DB 901 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
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 DB 961 TCCAGCC 967

RESULT 14
 ADL96477
 ID ADL96477 standard; CDNA; 1092 BP.

XX ADL96477;
 XX 20-MAY-2004 (first entry)
 XX Human G protein-coupled receptor (GPCR) cDNA #16.
 XX Human, G protein-coupled receptor; GPCR; gene; ss.
 XX Homo sapiens.
 XX US2003166148-A1.
 XX 04-SEP-2003.
 XX 16-DEC-2002; 2002US-00321807.
 XX 13-OCT-1998; 98US-00170496.
 XX 16-NOV-2000; 2000US-00714008.
 XX (CHEN/) CHEN R.
 XX (DANG/) DANG H T.
 XX (LOWI/) LOWITZ K P.
 XX Chen R, Dang HT, Lowitz KP;
 XX WPI; 2003-898073/82.
 XX P-PSDB; ADL96478.
 XX New G protein-coupled receptor (GPCR), useful for preparing a composition
 PT for identifying compounds as receptors, inverse agonists or partial
 PT agonists having potential applicability as therapeutic agents.
 XX Example 1; SEQ ID NO 31; 82pp; English.
 XX The invention relates to G protein-coupled receptor (GPCR) polypeptides
 CC and the polynucleotides encoding them. The GPCR polypeptides are useful
 CC for preparing a composition for identifying compounds as receptors,
 CC inverse agonists or partial agonists, having potential applicability as
 CC therapeutic agents. This sequence represents human GPCR cDNA of the
 CC invention.
 XX Sequence 1092 BP; 151 A; 397 C; 340 G; 204 T; 0 U; 0 Other;
 XX Query Match 41.2%; Score 418.2; DB 11; Length 1092;
 XX Best Local Similarity 64.5%; Pred. No. 6.8e-66;
 XX Matches 624; Conservative 0; Mismatches 343; Indels 0; Gaps 0;

```

QY 1 ATGAACCTGATGAGACGCGGCGCTGCGAGGCTACATGATGAGGAGGCTGCTGCTG
DB 1 ATGGGCCCCGGGCGAGGCGCTGCGCGGCTCTCTGGGATGATGAGGCTGCGGCTG
QY 61 CTGTTCACACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB 61 CTATTCACACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 121 CCGGCGGCTCTCACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAAC
DB 121 TCAGGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 181 CCGGCTCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTG
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QY 241 CTGAGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB 241 CTGAGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 301 AGCATTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB 301 AGCATTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 361 CCGGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB 361 CCGGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 421 GCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB 421 GCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 481 CCGGCGGCGAGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB 481 CCGGCGGCGAGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 541 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB 541 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 601 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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QY 721 AAGAGATCAGCACCCTTCAATGAGGACCTTCTGCTGCTGCTGCTGCTGCTGCTG
DB 721 AAGAGATCAGCACCCTTCAATGAGGACCTTCTGCTGCTGCTGCTGCTGCTGCTG
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DB 781 AGGCTGAGGAGCTTCTTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 841 AGGCTGAGGAGCTTCTTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB 841 AGGCTGAGGAGCTTCTTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 901 TACCGCAAAAGCTGCAAGGATTTCTGAACGCTCTGCAACGACGCTCAATCCATCC
DB 901 TACCGCAAAAGCTGCAAGGATTTCTGAACGCTCTGCAACGACGCTCAATCCATCC
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DB 961 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

```

RESURF 15
ABZ24430
ID ABZ24430 standard; cDNA; 5665 BP.

```

XX AC ABZ24430;
XX 18-MAR-2003 (first entry)
XX DE Human constitutively active receptor (hCAR) cDNA.
XX KW Constitutively active receptor; human; hCAR; receptor;
XX KM G-protein coupled receptor; cytosolic; neuroleptic; antiParkinsonian;
XX OS chromosome 4; gene therapy; gene; ss.
XX OS Homo sapiens.
XX FH Key
XX FH 5'UTR
XX FT 1.1891
XX FT 1892.2383
XX FT CDS
XX FT /*tag= b
XX FT /product= "human constitutively active receptor"
XX FT /note= "an isolated nucleic acid comprising the coding
XX FT region is specifically claimed in Claim 8"
XX FT 2984.5665
XX FT /*tag= c
XX PN WO2002101005-A2.
XX PD 19-DEC-2002.
XX XX 30-MAY-2002; 2002WO-US016834.
XX PF 07-JUN-2001; 2001US-0297131P.
XX PR (AMHP) WYETH.
XX PA Blatcher M, Bates BG, Paulsen JB;
XX PI WPI; 2003-148789/14.
XX XX P-PSDB; ABP58167.
XX DR New human constitutively Active Receptor (hCAR) gene, useful for
XX DR preparing a composition for treating disorders associated with aberrant
XX PT hCAR protein activity or hCAR nucleic acid expression, e.g., tumor or
XX PT schizophrenia.
XX PS Claim 7; Page 118-122; 139pp; English.
XX XX The present sequence is that of cDNA encoding the novel human
XX CC constitutively active receptor (hCAR) protein. hCAR is a G-protein
XX CC coupled receptor that is expressed predominantly in the brain and
XX CC placenta. The hCAR cDNA was isolated from a human cerebellum library. The
XX CC gene (see ABZ24431) is located in chromosome 4. The invention provides
XX CC hCAR nucleic acids and polypeptides, host cells, and methods of producing
XX CC the polypeptides and for detecting the nucleic acids. Also claimed are: a
XX CC method for identifying a compound that binds to hCAR protein; a method
XX CC for modulating the activity of the protein; a method for treating a
XX CC patient having the need for inhibition of hCAR activity; a transgenic,
XX CC chimeric, or knockout non-human animal comprising the present sequence;
XX CC and a method for inhibiting expression of the hCAR gene. The invention
XX CC also relates to improved methods for both the in vitro production of hCAR
XX CC protein and for the production and delivery of hCAR protein by gene
XX CC therapy. hCAR nucleic acids can also be used in diagnostic assays,
XX CC pharmacogenomics, chromosome mapping and tissue typing. An hCAR
XX CC gene/protein modulator, e.g., an antisense oligonucleotide or small
XX CC peptide, can be used to treat a disease or disorder associated with
XX CC abnormal or aberrant hCAR protein activity or hCAR nucleic acid
XX CC expression, especially a disorder involving the brain such as Parkinson's
XX CC disease or schizophrenia, or cancer
XX XX Sequence 5665 BP; 1084 A; 1654 C; 1635 G; 1292 T; 0 U; 0 Other;

```

Query Match 41.1%; Score 416.6; DB 10; Length 5665;
Best Local Similarity 64.4%; Pred. No. 1.4e-65;
Matches 623; Conservative 0; Mismatches 344; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:08:04 ; Search time 4630 Seconds
(without alignments)
10612.006 Million cell updates/sec

Title: US-10-735-991-5

Perfect score: 1014
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1014	100.0	1014	6	C0831055 Sequence
2	1011	99.7	1011	6	C0831051 Sequence
3	1010.8	99.7	7512	6	HSAS05757
4	1009.2	99.5	2581	6	BD130531
5	1006.2	99.2	1011	6	BD130532
6	967.4	95.4	969	6	C0729494
7	868.4	85.6	1172	6	C0831053
8	868.4	85.6	1172	6	C0831053
9	668.6	65.9	196808	9	AC009987
10	589.6	58.1	162502	10	AC105062
11	579	57.1	68539	2	AC099826
12	456.2	45.0	525	10	AY255585
13	418.2	41.2	1092	6	AX148190
14	416.6	41.1	1092	6	AX592452
15	416.6	41.1	1092	6	AX592450
16	415	40.9	1029	6	C0716319
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21	415	40.9	1092	6	AX670876
22	415	40.9	1092	6	BD095690
23	415	40.9	1092	9	BC069343
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26	415	40.9	1188	6	AX521989
27	415	40.9	1510	6	AX376522
28	415	40.9	1510	6	AX359107
29	415	40.9	1953	9	BC057778
30	415	40.9	3119	6	C0850655
31	415	40.9	3119	6	AK128807
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33	410.2	40.5	1092	9	AF411107
34	396	39.1	1361	6	AX670878
35	298.2	29.4	181601	2	BX927351
36	282.4	27.9	1000	6	AX670870
37	282.4	27.9	1059	6	AX375436
38	282.4	27.9	6784	6	AX646681
39	282.4	27.9	6784	9	AB065673
40	282.4	27.9	7020	6	AX316189
41	282.4	27.9	196902	9	AC105345
42	282.4	27.9	200000	2	AC007104
43	282.4	27.9	214284	9	AC116643
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45	267.2	26.4	657	6	AX147758

ALIGNMENTS

RESULT 1	CO831055	1014 bp	DNA	linear	PAT 29-JUL-2004
LOCUS	CO831055	Sequence 5 from Patent EP1437595.			
DEFINITION	CO831055				
ACCESSION	CO831055.1	GI:50831180			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
	Homo sapiens (human)				
	Homo sapiens				
REFERENCE					
AUTHORS	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.				
TITLE	Oryphan GPCR gene 115 for obesity indication				
JOURNAL	Patent: EP 1437595-A 5 14-JUL-2004;				
	F. HOFFMANN-LA ROCHE AG (CH)				
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Query Match	100.0%; Score 1014; DB 6; Length 1014;				
Best Local Similarity	100.0%; Pred. No. 76-124;				
Matches 1014; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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DB	1 ATGAACCTCGTGGAGCGCGGCTGCGGCGGCTA	CTGAGTGGGACGATGGGCGTCTCGCTG	60		
QY	61 CTGTCCACGCGCTGTGTCTCTCTCTCTCTCTCT	CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	120		
DB	61 CTGTCCACGCGCTGTGTCTCTCTCTCTCTCTCT	CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	120		
QY	121. CCGGCGCTCTTCACTCACTCACTCACTCACTCA	CTGAGTGGGACGATGGGCGTCTCGCTG	180		
DB	121 CCGGCGCTCTTCACTCACTCACTCACTCACTCA	CTGAGTGGGACGATGGGCGTCTCGCTG	180		
QY	181 CCGCTACGCTGGCGCGCGCTGTGTGTGTGTGT	GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	240		
DB	181 CCGCTACGCTGGCGCGCGCTGTGTGTGTGTGT	GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	240		

OY		241	CTGGCTGCTTCTTGACACTTCTCGGTGGCTAGCACTCATAGTCTAGCATGGCCGCCTC	300
Db		241	CTGGCTGCTTCTTGACACCCTTCCTGGCTGGCAAATCTCAAGTCATGAGATGGCCGCTC	300
OY		301	AGCATTCGACCGCTGGGTGGCCGTGGTTTCCCGCTGAGCTAACCGAGGCCAAAGTAGCGCTC	360
Db		301	AGCATTCGACCGCTGGGTGGCCGTGGTTTCCCGCTGAGCTAACCGAGGCCAAAGTAGCGCTC	360
OY		361	CGGACCGGGCGCTCATATGTTGGCTTAACGATGGCTGACAAGGCTTACCTTCCACCGCC	420
Db		361	CGGACCGGGCGCTCATATGTTGGCTTAACGATGGCTGACAAGGCTTACCTTCCACCGCC	420
OY		421	GCGCTCGCCCTCTCTCTGGCTGGCTTCCAACAAGCTGTAAGGCTGTGTGAAGCTGTGACG	480
Db		421	GCGCTCGCCCTCTCTCTGGCTGGCTTCCAACAAGCTGTAAGGCTGTGTGAAGCTGTGACG	480
OY		481	CGGCGGCGCAGAAGACGCGCTCGCTTCGCGCTTTCATGTGCGCGCTTCAAGCTTCAGC	540
Db		481	CGGCGGCGCAGAAGACGCGCTCGCTTCGCGCTTTCATGTGCGCGCTTTCAGCTTCAGC	540
OY		541	TTCCTGCTCTCTTGTGTTGTTGCTCTGTCAGTACCTCAAGGTGCTCAAGGTGGCCGC	600
Db		541	TTCCTGCTCTCTTGTGTTGTTGCTCTGTCAGTACCTCAAGGTGCTCAAGGTGGCCGC	600
OY		601	TTTCCATTGGCAAGCGCATGACGTATCACATGACAGACGCTGTGTGCTGTGTGACCTG	660
Db		601	TTTCCATTGGCAAGCGCATGACGTATCACATGACAGACGCTGTGTGCTGTGTGACCTG	660
OY		661	CACCCAGTGTGCGGGAACGCTGTCTGAGAGAGCAGAACGGAGCGACAGCCAGCCACC	720
Db		661	CACCCAGTGTGCGGGAACGCTGTCTGAGAGAGCAGAACGGAGCGACAGCCAGCCACC	720
OY		721	AAGAAGATCAGCACTTATATGAGAACCTTCTTGTGTGCTTGGCGCCTATATGTATCAC	780
Db		721	AAGAAGATCAGCACTTATATGAGAACCTTCTTGTGTGCTTGGCGCCTATATGTATCAC	780
OY		781	AGGCTAGTGAAGCTCTTCCACGGTGGCCATCCGCTCCCATGGGGGGTGTGTGTCAG	840
Db		781	AGGCTAGTGAAGCTCTTCCACGGTGGCCATCCGCTCCCATGGGGGGTGTGTGTCAG	840
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Db		841	TGCTTGGCGTACAGCAGAGCGCATCCGACCCTTGTGTATCTCCCTTACTGCGACACAG	900
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OY		961	TCTGGCTCAGAGGCGACTTCAACAGCAGAACTTCTGCGGTGTCTGAGTGA	1014
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DEFINITION	Sequence 1 from Patent EP1437595.			
ACCESSION	COB31051			
VERSION	COB31051.1		GI:50831178	
KEYWORDS				
SOURCE	Mus musculus (house mouse)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	Goodnow,J.R., Mark,D.F., Martin,M.L. and Rosinski,J.A. Orphan GPCR gene 115 for obesity indication Patent: EP 1437595-A 1 14-JUL-2004;			
AUTHORS	F. HOFFMANN-LA ROCHE AG (CH)			
JOURNAL	Location/Qualifiers			
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Matches 1011; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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OY	CTGACCAACGCGCGTGTGCTCTGCGCTGTGACACAGCGGGACATCCGCGCCAGCG	120
DB	CTGTCCAAAGCGCTGTGTGCTCTGCTGTGTCACAGCGGGACATCCGCGCCAGCG	120
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DB	121 CCGCGCGCTTCTCAACCTGAACCTGACGTCGGGAACTCTGTGTGACCCGTTGTCATATG	180
OY	181 CCGCTCACCGCTGCGCGGCTGTGTGGCGACGCGGACCGCGGCGACCGCTGTGCGC	240
DB	181 CCGCTCACGCTGCGCGGCTGTGTGGCGACGCGGACCGCGGCGACCGCTGTGCGC	240
OY	241 CTGGCTGCTTCTCCGACACCTTCTCTGGCTGACCACTCAGTCTCAGATGGCGCGCTC	300
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OY	301 AGCATTCGACCGCTGGGTGGCGGTGGTCTTCCCGCTGAGCTACCGGGCCAAATGGCGCTC	360
DB	301 AGCATTCGACCGCTGGGTGGCGGTGGTCTTCCCGCTGAGCTACCGGGCCAAATGGCGCTC	360
OY	361 CGCGACGCGGCGCTCATGTGTGGCTTCAAGTGGCTGACGCGCTCACCTTCCACGCGCC	420
DB	361 CGCGACGCGGCGCTCATGTGTGGCTTCAAGTGGCTGACGCGCTCACCTTCCACGCGCC	420
OY	421 GCGCTCGCGCTGCTCTGGCTGGCGCTTCCACGAGCTGATCGCTGTGACGCTGTGACG	480
DB	421 GCGCTCGCGCTGCTCTGGCTGGCGCTTCCACGAGCTGATCGCTGTGACGCTGTGACG	480
OY	481 CGGCGGCGACGACGCGCTGCGCTTCCGCGCTCTTCACTGGCGCTTCCAGCTTCAAGC	540
DB	481 CGGCGGCGACGACGCGCTGCGCTTCCGCGCTCTTCACTGGCGCTTCCAGCTTCAAGC	540
OY	541 TTCTGTCTCTCTTCTGTGTGCTCTGTGACGTAACCTCAAGGTGCTCAAGTGGCGCGC	600
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OY	901 TACGCAAAACCTGCAAGAGATTTCTGAACAGGCTCTGTCACAGACGCTCATCATCC	960
DB	901 TACGCAAAACCTGCAAGAGATTTCTGAACAGGCTCTGTCACAGACGCTCATCATCC	960
OY	961 TCTGGCTTCAAGGCGACTTTCACAGCCAGAACATTTCTCGGCTGTCTGAG	1011

Db 961 TCTGACCTCAGAGGACTCTCAAGCCAGAACATTCTGCGGTCTGAG 1011

RESULT 3
LOCUS HSA505757
DEFINITION Homo sapiens mRNA for putative orphan G protein-coupled receptor 26 (GPR26 gene).
ACCESSION AJ505757
VERSION AJ505757.1 GI:22293640
KEYWORDS GPR26 gene; orphan G protein-coupled receptor 26.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Boulay, J. L., Labuhn, M., Jones, G., Maier, D. and Merlo, A.
TITLE The 10q25.3-26.1 gene encoding the orphan G protein-coupled receptor GPR26 is epigenetically silenced in human gliomas
JOURNAL Unpublished
REFERENCE 2
AUTHORS Jones, G., Boulay, J. L., Maier, D. and Merlo, A.
TITLE Sequence of the human homologue of the rat orphan G protein-coupled receptor GPR26 mRNA
JOURNAL Unpublished
REFERENCE 3
AUTHORS Boulay, J. L.
TITLE Direct Submission
JOURNAL Submitted (13-ANG-2002) Boulay J. L., Research, University Hospital of Basel, 46 Schanzenstrasse, CH-4031 Basel, SWITZERLAND

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ORIGIN
Query Match 99.7%; Score 1010.8; DB 9; Length 7512;
Best Local Similarity 99.8%; Pred. No. 1,1e-123;
Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAACCTGAGGAGCGGGGCTGAGGAGGCTACTGAGGAGCAAGATGGCTTCGCTG 60
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Qy 61 CTGTCCAAACGCGCTGTGCTGTGCTGTGCTGCAAGCGGAGCATCCCGCCAGGCG 120
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Qy 121 CGGCGCTTCTTCACTGAACTCACTGCGGGAACCTGTGTGACCGTGTGTCATG 180

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RESULT 4
LOCUS BD130531
DEFINITION ligand receptors and utilization thereof.
ACCESSION BD130531
VERSION BD130531.1 GI:23225476
KEYWORDS JP 2002501083-A/1.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2581)
AUTHORS Glucksmann, A.W. and Robison, K.
TITLE ligand receptors and utilization thereof
JOURNAL Patent: JP 2002501083-A 1 15-JAN-2002;

COMMENT
MILLENNIUM PHARMACEUTICALS INC
OS Unidentified
PN JP 2002501083-A/1
PD 15-JAN-2002
PF 20-JAN-1999 JP 2000528599
PR 26-JAN-1998 US 09/013634
PI ALEXANDRA M GLUCKSMANN, KEITH ROBINSON
PC C07K14/705, C07K16/28, C12N5/10, C12N15/09, C12P21/02, C12Q1/68, PC
G01N33/53,
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Best Local Similarity 99.7%; Pred. No. 2.3e-123;
Matches 1011; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB AGCATTCAGCCGCTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
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BD130532 1011 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION
BD130532
ACCESSION
BD130532.1 GI:23225477
VERSION
BD130532.1
KEYWORDS
JP 2002501083-A/2.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 1011)
AUTHORS
Glucksmann, A.M. and Robison, K.
TITLE
Ligand receptors and utilization thereof
JOURNAL
Patent: JP 2002501083-A 2 15-JAN-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT
OS Unidentified
PN JP 2002501083-A/2
PD 15-JAN-2002
PF 20-JAN-1999 JP 2000528599
PR 26-JAN-1998 US 09/013634
PI ALEXANDRA M GLUCKSMANN, KEITH ROBINSON
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G01N33/53,
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CC Topology: Linear;
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Best Local Similarity 99.7%; Pred. No. 7.4e-123;
Matches 1008; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	1. ATGAACCTGCTGGGACGGGGGCTCTGGACGGGCTACTGATGGGACGATGGGCTCTGCTG 60
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	27 ATGAACCTGCTGGGACGGGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTG 86
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	61 CTGTCCAAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	87 CTGTCCAAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 146
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	121 CCGGCGCTCTTCAACCTGAACTCAACGCTGCGGAACTGCTGTGCAACGCTGTGCAACATG 180
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QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	207 CCACTTAACCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	241 CTGGCTGCTCTCTGACACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	267 CTGGCGCGCTCTCTGACACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 326
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	301 AGCATGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	327 AGCATGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 386
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	361 CCGGACGCGGCGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers	1..1172	387 CCGGACGCGGCGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 446
QY	CO831053	Sequence 3 from Patent EP1437595.	CO831053	CO831053.1	GI:50831179	Rattus norvegicus (Norway rat)	Rattus norvegicus	Goodnow, J.R., Mark, D.F., Martin, M.L. and Rosinski, J.A.	Orphan GPCR gene 115 for obesity indication	Patent: EP 1437595-A 3 14-JUL-2004;	F. HOFMANN-LA ROCHE AG (CH)	Location/Qualifiers		

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gene	1. .1172 /organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10116" /chromosome="10" /map="10q26.2-q26.3" 1. .1172 /gene="GPR26"
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QY		181	CCGCCTCAGCGTGGCGCGCGTGTGCGGACCGGCGGCGGACCGCCTGTGCC	240
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QY		241	CTGGCTGCTTCTCTGACAATTCTTGGTGCCAATCTCATGTCTAGCATTTGGCCGGCTC	300
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LOCUS		162502 bp	DNA linear	ROD 26-JUN-2004
DEFINITION	Mus musculus chromosome 7, clone RP24-528B17, complete sequence.			
ACCESSION	AC105062			
VERSION	AC105062.13	GI:49258241		
KEYWORDS	HTG.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	1 (bases 1 to 162502)			
JOURNAL	Birren, B., Nuebaum, C. and Lander, E.			
REFERENCE	Mus musculus chromosome 7, clone RP24-528B17			
AUTHORS	Unpublished			
	2 (bases 1 to 162502)			
	Birren, B., Linton, L., Nuebaum, C., Lander, E., Ali, A., Allen, N.,			
	Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,			
	Brown, A., Camarata, J., Campioano, A., Chang, Y., Chiaro, B.,			
	Chopel, Y., Colangelo, M., Collins, S., Collimore, A., Cook, A.,			
	Cooke, P., Dearellano, K., Dewar, R., Diaz, J.S., Dodge, S., Fato, S.,			
	Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,			
	Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,			
	Hagde, B., Heatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,			
	Jones, C., Kamat, A., Karatas, A., Kelis, C., LaRoque, K.,			
	Lamaizares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,			
	Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C.,			
	McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Melidim, J.,			
	Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,			
	Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,			
	Oliver, J., Peterson, K., Phumhang, P., Pierre, N., Pollatz, V.,			
	Raymond, C., Retta, R., Ribbeck, M., Riley, R., Rise, C., Rogov, P.,			

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talama, J., Tesfaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Triggilo, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (23-DEC-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 162502)
 Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N.,
 Anderson, M., Anderson, S., Archchi, H. M., Barna, N., Bastien, V.,
 Bloom, T., Boguslavsky, L., Bookbalter, B., Camarata, J., Chang, J.,
 Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B.,
 DeRellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L.,
 Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,
 Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,
 Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,
 Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T.,
 Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
 Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C.,
 McCarthy, M., Meldrim, J., Meneses, L., Mihova, T., Menga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,
 O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
 Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
 Reata, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R.,
 Sema, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Stubbs, M., Talama, J., Tesfaye, S., Theodore, J.,
 Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R.,
 Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
 Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (22-APR-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 162502)
 Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N.,
 Anderson, M., Anderson, S., Archchi, H. M., Barna, N., Bastien, V.,
 Bloom, T., Boguslavsky, L., Bookbalter, B., Camarata, J., Chang, J.,
 Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B.,
 DeRellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L.,
 Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,
 Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,
 Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,
 Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T.,
 Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
 Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C.,
 McCarthy, M., Meldrim, J., Meneses, L., Mihova, T., Menga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,
 O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
 Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
 Reata, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R.,
 Sema, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Stubbs, M., Talama, J., Tesfaye, S., Theodore, J.,
 Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R.,
 Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
 Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (26-JUN-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 26, 2004 this sequence version replaced gi:46485957.
 All repeats were identified using RepeatMasker:
 Smt, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@broad.mit.edu
 ----- Project Information
 Center project name: 117510
 Center clone name: 528_E_17
 ----- Location/Qualifiers

Qy 661 CACCCGAG 668
 Db 25724 CACCCGAG 25717

RESULT 11
 AC099826 68539 bp DNA 1linear HTG 30-JUL-2002
 LOCUS AC099826
 DEFINITION Papio hamadryas clone RP41-76M19, LOW-PASS SEQUENCE SAMPLING.
 AC099826.2 GI:22004220
 VERSION HTG; HTS_PHASE0.
 KEYWORDS Papio hamadryas (hamadryas baboon)
 SOURCE Papio hamadryas
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.

REFERENCE 1 (bases 1 to 68539)
 AUTHORS Birren,B., Nusbaum,C. and Lander,E.
 TITLE Papio hamadryas, clone RP41-76M19
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 68539)
 AUTHORS Birren,B., Linton,J., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A., Camarata,J., Campiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,W., Graham,W., Grand-Pierre,N., Hagos,B., Hatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kellis,C., Lacroque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., Mcswan,P., McKernan,K., McPheeters,R., Meldrim,J., Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunhahng,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N., Strassman,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H., Vei,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission
 JOURNAL Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 68539)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,W., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kellis,C., Levine,R., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., MacDonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunhahng,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Vei,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission
 JOURNAL Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT On Jul 30, 2002 this sequence version replaced gi:117047165. All repeats were identified using RepeatMasker: http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: MIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L12534
 Genet clone name: 76_M_19

 * NOTE: This record contains 85 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

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16111	16820: contig of 710 bp in length
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19327	20044: contig of 718 bp in length
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Oy		121	CCGGCGCTTTTCAACCCGGAAGCCTCAAGTGAGGGAACTGTGTCATGCACCGGTGTCAACTATG	180
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Db		11862	TTCCTGTGCTTCTCTTTCGTGCTGCTGTCTGTGTCAGTACGTAAAGGAGTCTCAAGTGTGCCCC	11922
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LOCUS	AY255585			
DEFINITION	Mus musculus G protein-coupled receptor GPR26 mRNA, partial cds.			
ACCESSION	AY255585			
VERSION	AY255585.1			
KEYWORDS	GI:29611571			
SOURCE				
ORGANISM	Mus musculus (house mouse)			
REFERENCE				
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus,			
	1 (bases 1 to 525)			
	Vassiliadis,D.K., Hohmann,J.G., Zeng,H., Li,F., Ranchalis,J.E.,			
	Mortrud,M.T., Brown,A., Rodriguez,S.S., Weller,J.R., Wright,A.C.,			
	Bergman,J.E. and Galitanaris,G.A.			
	The G Protein-Coupled Receptor Repertoires of Human and Mouse			
	Proc. Natl. Acad. Sci. U.S.A. 100 (8), 4903-4908 (2003)			
	2 (bases 1 to 525)			
TITLE				
JOURNAL				
REFERENCE				
AUTHORS				
	Vassiliadis,D.K., Hohmann,J.G., Zeng,H., Li,F., Ranchalis,J.E.,			
	Mortrud,M.T., Brown,A., Rodriguez,S.S., Weller,J.R., Wright,A.C.,			
	Bergman,J.E. and Galitanaris,G.A.			
	Direct Submission			
	Submitted (14-MAR-2003) Primal, Inc., 1124 Columbia Street,			
	Seattle, WA 98104, USA			
TITLE				
JOURNAL				
FEATURES				
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	/mol_type="mRNA"			
	/db_xref="taxon:10090"			
CDS	<1..>525			

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Best Local	Similarity	97.9%	Pred.	No. 2.5e-67				
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Qy	1	ATGAACTCTGTGGACGCGGGGCTTGACGGGCTCTCTGTGGGACGATGGGCGCTTGGCTG	60					
Db	11322	ATGAACTCTGTGGACGCGGGGCTTGATGGGCTGTGGGACGATGGGCGCTTGGCTG	11381					
Qy	61	CTGTCCAAACGCGCTGTGCTGTCTCTGCTCTGTCACAGCGGAGACATCCGCGCCAGAGG	120					
Db	11382	CTGTCCAAACGCGCTGTGCTGTCTCTGCTCTGTCACAGCGGAGACATCCGCGCCAGAGG	11441					

RRDRLRFAVTSAPFALSFLISFIVLCFTYLVKLVKVAEFHCKRIDVTMTQTLVLLV
DHPSTRECLJEOKRRORRATKKISTFISTFVLCFAPYVITLVELFSTAPIGSHWG
VLSKCLAVSKASADP"

ORIGIN

Query Match 45.0%; Score 456.2; DB 10; Length 525;
Best Local Similarity 91.8%; Pred. No. 1.2e-50;
Matches 482; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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DB 1 AAGATGGCTCCGCGCAGCGGCGCTCATGTGGCCCTACAGGTGGCGGCGCTACCC 60
QY 409 TTCCCAAGCCCGCGCTCGGCTGTCTGTGGCTGGCTTCCACAGCTGTAGCTCGTGC 468
DB 61 TTCCCGGCGCAGCGGCGCTCGGCTGTCTGTGGCTGGCTTCCACAGCTGTAGCTCGG 120
QY 469 AGCGTGTGACGCGGCGGCGCAGACGCGCTGTGGCTGGCTTCCACTGGCGCTTC 528
DB 121 ACAGTGTGACGCGGCGGCGCAGACGCGCTGTGGCTGTGTCTTCCACGCGCTTC 180
QY 529 CAGGCTGTGAGCTTCTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
DB 181 CAGGCTGTGAGCTTCTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 589 AAGGTGCGCGCTTCCATTGCAAGCGCATCGAGTGTATCAACATGACAGCGTGTGTG 648
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QY 649 CTGTGTGACCTGCAACCCCACTGTGTGGGAAAGCTGTGTGAGAGCAAGAGCGGAG 708
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QY 709 CAGGAGCGCACAAGAGATCAGACCTTATAGGAGCTTCTGTGTGTGTGTGTGTGTGT 768
DB 361 CAGGAGCGCACAAGAGATCAGACCTTATAGGAGCTTCTGTGTGTGTGTGTGTGTGT 420
QY 769 TATGTATACACAGGCTAGTGAAGCTTCTTCCACGCGTGCCTCGGCTCCACCTGG 828
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DB 481 GTGTGTGCAAGTGTGTGGGTACAGCAAGCGCGCATCCAGCC 525

RESULT 13
AX148190 1092 bp DNA linear PAT 08-JUN-2001
LOCUS AX148190
DEFINITION Sequence 31 from Patent WO0136471.
ACCESSION AX148190
VERSION AX148190.1 GI:14347088

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
AUTHORS Chen, R., Dang, H. T. and Lowitz, K. P.
TITLE Endogenous and non-endogenous versions of human g protein-coupled
JOURNAL Patent: WO 0136471-A 31 25-MAY-2001;
ARENA Pharmaceuticals, Inc. (US)
FEATURES location/Qualifiers
SOURCE 1. 1092
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 41.2%; Score 418.2; DB 6; Length 1092;
Best Local Similarity 64.5%; Pred. No. 9.3e-46;
Matches 624; Conservative 0; Mismatches 343; Indels 0; Gaps 0;

QY 1 ATGAACTCGTGGAGCGCGGCGCTGGCGGCGCTAATGTGGGCAAGATGGGCGCTTCGCTG 60
DB 1 ATGAGCGCGGAGGCGCGCTGGCGGCGCTTCCTGTATGTATGTGACCGCGGCGCTG 60

QY 61 CTGTCCAAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 61 CTATTCBAAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 CCGGCGCTCTTCAACCTTGAACCTCAGGTGGGAACTGTGTGTGTGTGTGTGTGTGTGT 180
DB 121 TCAGGCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 181 CCGCTACGCTGTGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 181 CCGCTACGCTGTGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 241 CTGGCTGCTTCTCTCAACACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 241 GTCAATGTGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 301 AGCATGACGCGTGGGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 AGCGAGACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 CCGGAGCGGCGCTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 361 CGCTATGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 421 GCGCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB 421 GCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 481 CCGCGCGCAGACGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 481 CCGCGCGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 541 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 541 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 601 TTCTATTTGCAAGGCTATCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 601 AGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
QY 661 CACCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 661 CACCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
QY 721 AAGAAATACAGCACTTCAATAGGAACTTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 721 AAGAAATGTGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
QY 781 AGGCTATGTGAGCTTCTTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
DB 781 AGGCTGTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 841 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 TTACGCAAAAGCTGTCAAGAGATTTGAAACAGGCTCTGTGACAGAGCTTCATCTCC 960
DB 901 TTCCGCAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY 961 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
DB 961 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967

RESULT 14
AX592452 1092 bp DNA linear PAT 27-JAN-2003
LOCUS AX592452


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DEFINITION Sequence 9 from Patent WO0232962.
ACCESSION AX592452
VERSION AX592452.1 GI:27950554
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1. Gluckmann, M.A. and Meyers, R.
    80090, 52874, 52880, 63497, and 33425 methods and compositions of
    human proteins and uses thereof
    Patent: WO 0232962-A 9 25-APR-2002;
    Millennium Pharmaceuticals, Inc. (US)
FEATURES
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    /mol_type="unassigned DNA"
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Query Match      41.1%; Score 416.6; DB 6; Length 1092;
Best Local Similarity 64.4%; Pred. No. 1.5e-45;
Matches 623; Conservative 0; Mismatches 344; Indels 0; Gaps 0;

QY 1 ATGAACCTGTTGAGAGCGCGGCTGAGCGGCTACTGTGGGCAAGATGGCGTCTG 60
Db 1 ATGGGCCCCGGAGGCGCTGCGGGGCTTCTGTGGATGATGATGCGCGCTGCG 60
QY 61 CTGTCCAAAGCGGTGTGTCTGTCTGCTGTGTGCAAGCGGGAATCCCGCCAGGCG 120
Db 61 CTATCCAAAGCGAGTGTGTCTGTCTGTGTGCGCCCTCAAGCGCTGAGCTCCGATCTGAGCC 120
QY 121 CCGGCGCTCTTCAACCTGAACTCAGCGTGGGGAACCTGCTGTGCAAGCGTGTCAACATG 180
Db 121 TCAGGCTCTCTCTGTGTGAACTCTCTGCTGGGCACTGTCTGTGGGCGGCTGAGCATG 180
QY 181 CCGGCTCAGCTGCGCGGCTGTGTGCGCAAGCGGAGCGCGGCGGCGAGCCGCTGTGCGC 240
Db 181 CCTTTCAGCTGCTGCGGCTGTGTGCGGCGGCGAGCACGTCGCGCGCGGCGCATGCGAA 240
QY 241 CTGGCTGCTCTCTCTGCAACCTTCTGTGTGCTGCAATCTCATGTCTGAGATGCGCGCTC 300
Db 241 GTCAATGCTCTCTGCAACCTTCTGTGCGCTCAACCGCGCTGAGCGTGTGCGCGCTG 300
QY 301 AGCATCAGCGCTGGTGTGCGCGTGTCTTCCGCTGAGCTAACCGGCGCAAGATGGCGCTC 360
Db 301 AGCGCAGACAGTGTGTGCGAGTGTGCTTCCCACTGCGCTAACCGCGAGCGCTGCGACCG 360
QY 361 CCGGACCGCGGCTCATGTGTGCTTACAGCGTGTGCAAGCGGCTCACTTCCAGCGCGC 420
Db 361 CGGTATGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 421 GCGCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db 421 GCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 481 CCGGCGCGCAGAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db 481 CCGGCGCGCAGAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 541 TTGCTGTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
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QY 661 CACCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 661 CACCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720

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QY 721 AAGAAGTACAGCACTTCAATAGGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
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QY 781 AGGCTAGTGAAGCTCTTCTCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 781 AGGCTAGTGAAGCTCTTCTCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 841 TGCTTGGCTGACAGCAAGCGCGATCCGACCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 841 TGCTTGGCTGACAGCAAGCGCGATCCGACCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 TACCGCAAAAGCTGCAAGAGATTTGGAACAGGCTCTGTGCAAGAGCGCTTCATCTCC 960
Db 901 TACCGCAAAAGCTGCGCGGATGTGCAAGAGGCTGTGGAAGAACCCCGCGCCAGCA 960
QY 961 TCTGTGCGC 967
Db 961 TCCACCC 967

RESULT 15
AX592450 1352 bp DNA linear PAT 27-JAN-2003
LOCUS
DEFINITION Sequence 7 from Patent WO0232962.
ACCESSION AX592450
VERSION AX592450.1 GI:27950552
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1. Gluckmann, M.A. and Meyers, R.
    80090, 52874, 52880, 63497, and 33425 methods and compositions of
    human proteins and uses thereof
    Patent: WO 0232962-A 7 25-APR-2002;
    Millennium Pharmaceuticals, Inc. (US)
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    DQMLAVGFLPRLVAGRLPRYAGLLGCMGOSLAFSGALGCSMLGYSSAFASLRL
    PEPBPBPRAATPATTHAANGPVLPLAVLCISIQYRVARSHQRPDPTMKALALA
    DHPBSVROKLIQKRRHRAIRKIGIALATFLICFAPYVMTLAEVLPVTVAQMG
    ILSKLCITYSKAVADPFTYSLRRPFQGVAVGWRLKTRPPASTHDSLDVAGVH
    QLKRTTRPASTHDSVTDENDSCLOQT"
ORIGIN
Query Match      41.1%; Score 416.6; DB 6; Length 1352;
Best Local Similarity 64.4%; Pred. No. 1.4e-45;
Matches 623; Conservative 0; Mismatches 344; Indels 0; Gaps 0;

QY 1 ATGAACCTGTTGAGAGCGCGGCTGAGCGGCTACTGTGGGCAAGATGGCGTCTG 60
Db 210 ATGGGCCCCGGAGGCGCTGCGGGGCTTCTGTGGATGATGATGCGCGCTGCG 269
QY 61 CTGTCCAAAGCGGTGTGTCTGTCTGCTGTGTGCAAGCGGGAATCCCGCCAGGCG 120
Db 270 CTATCCAAAGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 329
QY 121 CCGGCGCTCTTCAACCTGAACTCAGTGTGCGGAACCTGTGTGCAACCGTGTGCAATG 180
Db 330 TCAGGCGCTCTCTGTGTGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 389

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QY	112	CGCCAGGAGCGCGGCGCTTTCA	CGCTTGAACCTTCAAGTGGGGAA	CTGGCTGTGACCGTG	171			
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QY	172	GTCAACATGCGGCTCA	CGCTGAGCGGCGTGTGGCGAGCGGACGCG	CGCGCGGACGCG	231			
Db	121	GTCAACATGCGGCTCA	CGCTGAGCGGCGTGTGGCGAGCGGACGCGCGGCGGACGCG		180			
QY	232	CTGTGCGCGCTGAGCTTGC	CTTGCACACTTCCGTGGCTGC	CAATCTCAGATG	291			
Db	181	CTGTGCGCGCTGAGCTTGC	CTTGCACACTTCCGTGGCTGC	CAATCTCAGATG	240			
QY	292	GCCGCGCTCAGACTGAC	CGCTGGGTGGCGGTGTCTTCCGCTGAGCT	ACCGGGCCAG	351			
Db	241	GCCGCGCTCAGACTGAC	CGCTGGGTGGCGGTGTGTCTTCCGCTGAGCT	ACCGGGCCAG	300			
QY	352	ATGGGCGCTCGGCGAG	CGGGGGGCTAGTGGTGGCTA	CATGGGCTGCAGCGCTCACCTTC	411			
Db	301	ATGGGCGCTCGGCGAG	CGGGGGGCTAGTGGTGGCTA	CATGGGCTGCAGCGCGCTCACCTTC	360			
QY	412	CCAGCGCGCGGCTCG	CGCTGTCTGAGCTCGAGCTTCCACAGCTTGAAGCCTCGTGC	ACG	471			
Db	361	CCAGCGCGCGGCTCG	CGCTGTCTGAGCTCGAGCTTCCACAGCTTGAAGCCTCGTGC	ACG	420			
QY	472	CTGTGACCGGCGGCGAG	CGAGCGCTGCGCTTGC	CGCTTTCATGTGCGCTTCCAC	531			
Db	421	CTGTGACCGGCGGCGAG	CGAGCGCTGCGCTTGC	CGCTTTCATGTGCGCTTCCAC	480			
QY	532	GCTCTCAGCTTCTGCT	CTCTCTGTGCTGTCTCTGTGCTGCA	AGTACCTGAAGTGTGCAAG	591			
Db	481	GCTCTCAGCTTCTGCT	CTCTCTGTGCTGTCTCTGTGCTGCA	AGTACCTGAAGTGTGCAAG	540			
QY	592	GTGGCGCGCTTCAT	TGGAGGAGATCGACGATCA	CCATGACAGCGCTGATGCTGCTG	651			
Db	541	GTGGCGCGCTTCAT	TGGAGGAGATCGACGATCA	CCATGACAGCGCTGATGCTGCTG	600			
QY	652	GTGGACCTGCACCCCA	GTGTGCGGGAA	CGCTGTCTGGAAGGAGAGAA	CGGAGCGACG	711		
Db	601	GTGGACCTGCACCCCA	GTGTGCGGGAA	CGCTGTCTGGAAGGAGAGAA	CGGAGCGACG	660		
QY	712	CGAGCCACCAAGAA	GATCAGCACTTCA	TAGGAGCCTTCTTGTGTCTTGTGCGCCTTAT	771			
Db	661	CGAGCCACCAAGAA	GATCAGCACTTCA	TAGGAGCCTTCTTGTGTGTCTTGTGCGCCTTAT	720			
QY	772	GTGATCACA	CAAGCTAGTGAGCTTCTTCCACG	GTGGCCATTCGCTCCAC	CTGGGGGGGTG	831		
Db	721	GTGATCACA	CAAGCTAGTGAGCTTCTTCCACG	GTGGCCATTCGCTCCAC	CTGGGGGGGTG	780		
QY	832	CTGTGCAAGTCTTGG	CGCTTACAGCAAGGCGCGATTC	CGACCCCTTGTGTATCTCTTACTG	891			
Db	781	CTGTGCAAGTCTTGG	CGCTTACAGCAAGGCGCGATTC	CGACCCCTTGTGTATCTCTTACTG	840			
QY	892	CGACA	CCAGTACCGGAAAGCTG	CAAGAGATTTCTGAA	CAGGCTCTGCA	CGAGCGCTCC	951	
Db	841	CGACA	CCAGTACCGGAAAGCTG	CAAGAGATTTCTGAA	CAGGCTCTCTGCA	CGAGCGCTCC	900	
QY	952	ATTCACCTCTCTGG	CTCA	CAGGCGAC	CTCTCA	CAGCCGAA	CATTCTGCGGTGTCTGAG	1011
Db	901	ATTCACCTCTCTGG	CTCA	CAGGCGAC	CTCTCA	CAGCCGAA	CATTCTGCGGTGTCTGAG	960
QY	1012	TGA	1014					
Db	961	TGA	963					

RESULT 2	
AK036100	
LOCUS	2802 bp mRNA linear HMC 03-APR-2004
DEFINITION	Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
	enriched library, clone:9630036a11 Product:ORFAN G PROTEIN-COUPLE
	RECEPTOR GPR26 homolog [Rattus norvegicus], full insert sequence.
ACCESSION	AK036100

KEYWORDS	AK036100.1 GI:26331149
REVISION	HTC: CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	99279253
REFERENCE	10349636
AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komori, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	20499374
REFERENCE	11042159
AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komori, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishibe, T., Harada, A., Yamamoto, R., Watanabe, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E., Matsuki, M., Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzawa, S., Kawai, J., Yonezaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	20530913
REFERENCE	11076661
AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
PUBMED	11076661
REFERENCE	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
PUBMED	6 (Bases 1 to 2802)
REFERENCE	Aizawa, K., Akimura, T., Arai, A., Bono, H., Carninci, P., Adachi, S., Furuta, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizume, K., Hirooka, T., Hirose, T., Horii, F., Imokawa, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M., Koyama, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numata, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sobue, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
	Please visit our web site for further details.
	URL: http://genome.gsc.riken.jp/
	URL: http://fantom.gsc.riken.jp/

Db	1	GTGTCTGCTGTCTTCAACGAGCTGTGTGTCTGTCTGTCTGTCTGTGACACGCGCTGACATCCGC	60
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QY	172	GTCAACATGCGCTCACGCTGCGCGCGGTGTGTGGGCGACGCGGCGGCGGAGACCGC	231
Db	121	GTCAACATGCGCTTAACTAGTGGCGGCGGTGTGGGACACGCGGCGGCGGAGACCGC	180
QY	232	CTGTGCGCGCTGTGCGCTTCTCTGACACTTCTGTGTGCAACTCCATGCTCAGATG	291
Db	181	CTGTGCGCGCTGTGCGCTTCTCTGACACTTCTGTGCGCGCACTCCATGCTCAGATG	240
QY	292	GCGCGCTCAGCAATGACCGCTGTGGGTGGCGGTGTCTTCCGCTGAGGTACCGGGCCAG	351
Db	241	GCGCGCTCAGCAATGACCGCTGTGGGTGTGGGTCTTCTGCGTGAAGTACCGGTCCAG	300
QY	352	ATGCGCTCCGCGACGCGCGCGCTCATGTGTGCTCAACAGTGGCTGACGCGCTCACTTC	411
Db	301	ATGCGCTCCGCGAATGCGCGCTTCAATGTGTGCTCAACAGTGGCTGACAGCGCTCACTTC	360
QY	412	CCAGCGCGCGCTGTGCGCTTGTCTGTGCTGTGCTTCCACGACTGTACGCTGTGTACG	471
Db	361	CCGCGCTCAGCGCTGTGCGCTTGTCTGTGCTGTGCTTCCACGACTGTATAGCTGTGTGACA	420
QY	472	CTGTGCGACGCGGCGCGCGACGAGCGCGCTGTGCGCTTCCGCGCTTCACTGTGGCGCTTCCAC	531
Db	421	CTGTGCGACCGCGCGCGCGCGAGCGCGCTGTGCGCTTGTGTGCTTCTTCACTGAGGCGCTTCCAT	480
QY	532	GCTGTCAAGCTTCTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	591
Db	481	GCGCTCAGCTTCTGTCTGTCTTCTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540
QY	592	GTTGCGCGCGCTTCCATGTGCAAGCGCATGAGTGAATACACATGACAGCGCTGTGTGTGTGT	651
Db	541	GTTGCGCGCGCTTCCACTGTCAAGCGCATGAGTGAATACACATGACAGCGCTGTGTGTGTGT	600
QY	652	GTGGAACCTGCAACCCAGTGTGCGGGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	711
Db	601	GTGGAACATACACCCAGTGTGAGGGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	660
QY	712	CGAGCGACCAAGAAATATGACACTTCAATAGGAACCTTCTTGTGTGTGTGTGTGTGTGTGT	771
Db	661	GCTGCGCAACCAAGAAATATGACACTTCAATAGGAACCTTCTTGTGTGTGTGTGTGTGTGT	720
QY	772	GTGATTCACAGAGCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	831
Db	721	GTGATTCACAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
QY	832	CTGTTCGAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	891
Db	781	CTGTTCGAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	840
QY	892	CGACACCGATGACCGGAAAGCTGTGCAAGGAAATTCGAACAGGCTCTGTGACAGACGCTCC	951
Db	841	CGACACCGATGACCGGAGAGCTGTGCAAGGAAATTCGAACAGGCTCTGTGACAGAGCTCC	900
QY	952	ATTCACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1011
Db	901	CTTCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	960
QY	1012	TGA 1014	
Db	961	TGA 963	

RESULT 4	AY420106	666 bp	DNA	linear	GSS 12-DEC-2003
LOCUS	AY420106				
DEFINITION	Pan treglobulins HCMW113 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				

ACCESSION	AY420106
VERSION	AY420106.1 GI:39776063
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
AUTHORS	1 (bases 1 to 666) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Cjvello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 666)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Cjvello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence as made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1..666 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" <1..>666 /locus_tag="HCM7113"
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Best Local Similarity	83.9%; Pred. No. 1e-106;
Matches	559; Conservative 0; Mismatches 107; Indels 0; Gaps 0.

Db	481	CAAGGTGCTCAAGGTGCCCCGCTTCATTGCAGAGGCATCGACGTGATCACCATTGCAGAC	540
Qy	639	GCTGCTGCTGCTGCTGTGAGACTTGACCCCAAGTGTCTGGGAAACGCTGTCTTGAGAGAGCAGAA	698
Db	541	GCTCTGCTGCTGCTGTGAGACTTGACCCCAAGTGTGCGGAAACGCTGTCTTGAGAGAGCAGAA	600
Qy	699	GCGAGGGGAGCAGCCAGGCCACCCAAAGATCAGGCACCTTCATATGGGACCTTCTTGTTGTG	758
Db	601	GCGAGGGGAGCAGCCAGGCCACCCAAAGATCCTTCATATGGGACCTTCTTGTTGTG	660
Qy	759	CTTGGC 764	
Db	661	CTTGCC 666	

RESULT 5					
C0934052					
LOCUS	C0934052	741 bp	mRNA	linear	EST 16-AUG-2000
DEFINITION	AGENCOURT 30488535 NIH MGC 145 Homo sapiens CDNA clone				
	IMAGE:7262026 5', mRNA sequence.				

ACCESSION	CO9334052
VERSION	CO9334052.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

SOURCE ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE	1 (bases 1 to 741)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S. Gerhard, Ph.D.

FEATURES
source
Email: CSapbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: RB16 row: C column: 08
High quality sequence stop: 607.
Location/Qualifiers
1. .741

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7262026"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_1ib="NH1_MGC_145"
/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-ScorV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clone represents, please visit our anonymous ftp site at ftp://image.lnl.gov/image/rearrayed_plates/IRRI.presv.dat/a Note: this is a NH1_MGC library."

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Query Match 53.1%, Score 538.8; DB 7; length 741;
 Best Local Similarity 95.9%; Pred. No. 7.7e-103;
 Matches 585; Conservative 0; Mismatches 22; Indels 3; Gaps 3;

1 ATGAACCTGTGGGACGCGGCGCTTGGCGGGGCTACTGTGTGGGACGATGGCGGCTCTCGCTG 60
 16 ATGAACCTGTGGGACGCGGCGCTTGGCGGGGCTACTGTGTGGGACGATGGCGGCTCTCGCTG 75

QY	61	TTGTTCGAACGGGCTGTGTGTCTGTGCTGCGTGGCGTGCACAGGCGGGACATCCGCGCCAGGGG	120
Db	76	CTGTTCGAACGGGCTGTGTGTGTCTGTGCTGTGCACAGGCGGGACATCCGCGCCAGGGG	135
QY	121	CCGGGCGCTTTCACCCCTGAACCTCAAGTGGGGAACTTGCTGTGCACCCCTGTGCACATG	180
Db	136	CCGGGCGCTTTCACCCCTGAACCTCAAGTGGGGAACTTGCTGTGCACCCCTGTGCACATG	195
QY	181	CCGCTCAACGCTTGGCCGGGCGTGTGGCGCAAGCGGCAAGCGGCGGGCGGACCGCTGTGCCG	240
Db	196	CCGCTCAACGCTTGGCCGGGCGTGTGGCGCAAGCGGCAAGCGGCGGGCGGACCGCTGTGCCG	255
QY	241	CTGGCTGTGCTTCTCTCGAACCTTCCGTGGCTGGCACTCAATGCTACAGATGGCCGGGCTC	300
Db	256	CTGGCTGTGCTTCTCTCGAACCTTCTGGCTGGCACTCAATGCTACAGATGGCCGGGCTC	315
QY	301	AGCATTCGACCGCTGGGTGGCGGTGGTCTTCCCGCTGAGCTACCGGGCCAAAGATGCGCTC	360
Db	316	AGCATTCGACCGCTGGGTGGCGGTGGTCTTCCCGCTGAGCTACCGGGCCAAAGATGCGCTC	375
QY	361	CGCGACGCGGCGCTCATAGTGGCTTACAGTGGCTGCACAGGCTTCACTTCCAGCGCC	420
Db	376	CGCGACGCGGCGCTCATAGTGGCTTACAGTGGCTGCACAGGCTTCACTTCCAGCGCC	435
QY	421	GCGCTCGGCTGTCTCCGTGGCTGGCTTTCACACAGCTGTACGCTCGTGCACGCTGGCAAC	480
Db	436	GCGCTCGGCTGTCTCCGTGGCTGGCTTTCACACAGCTGTACGCTCGTGGCAAC	495
QY	481	CGGCGGCGAGAGCGCTGCGCTGCTCGGCGCTTCACTGGCGGCTTCCAGCTCTCAGC	540
Db	496	CGGCGGCGGAGAGCGCTGCGCTGCTCGGCGCTTCACTGGCGGCTTCCAGCTCTCAGC	554
QY	541	TTCTCTGCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	600
Db	555	-TCTGCTCTCTT-TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	612
QY	601	TTTCATTGCA 610	
Db	613	TTGCAAGCGCA 622	

RESULT 6	
CO934490	
LOCUS	736 bp mRNA linear EST 16-AUG-200
DEFINITION	IMAGCOURT 3048853 NIH_MGC_145 Homo sapiens cDNA clone
	IMAGE:7211818 5' mRNA sequence.
ACCESSION	CO934490
VERSION	CO934490.1 GI:51289167
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	1. (bases 1 to 736)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S. Gerhard, Ph.D.

CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
plate: RB15 row: c column: 08
High quality sequence stop: 600.
Location/Qualifiers
1..736

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_1lb="NIH_MGC_145"
/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XbaI/XhoI-3', 5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat a Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match      51.5%; Score 521.8; DB 7; Length 736;
Best Local Similarity 97.9%; Pred. No. 2.9e-99;
Matches 560; Conservative 0; Mismatches 8; Indels 4; Gaps 3;

QY 1 ATGAACCTGCTGGAGACGGGGCTGAGCGGGCTACTGCTGGGACAGATGGGCGTCTGCTG 60
DB 16 ATGAACCTGCTGGAGACGGGGCTGAGCGGGCTACTGCTGGGACAGATGGGCGTCTGCTG 75
QY 61 CTGTCCAAACGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 76 CTGTCCAAACGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 135
QY 121 CCGGCGCTCTTACACCTGAACTTCACTGCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 136 CCGGCGCTCTTACACCTGAACTTCACTGCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 195
QY 181 CCGGCGCTCTTACACCTGAACTTCACTGCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 196 CCGGCGCTCTTACACCTGAACTTCACTGCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 255
QY 241 CTGGCTGCTCTCTCTGCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 256 CTGGCTGCTCTCTCTGCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
QY 301 AGCATGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 316 AGCATGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
QY 361 CCGGCGCTCTTACACCTGAACTTCACTGCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 376 CCGGCGCTCTTACACCTGAACTTCACTGCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
QY 421 GCGCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 436 GCGCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
QY 481 CCGGCGCTCTTACACCTGAACTTCACTGCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 496 CCGGCGCTCTTACACCTGAACTTCACTGCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
QY 541 TTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
DB 554 TTC--TGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583

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RESULT 7

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CO934461/c      730 bp      mRNA      linear      EST 16-AUG-2004
LOCUS           CO934461
DEFINITION      AGENCOURT 30698355 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7211818 3', mRNA sequence.
ACCESSION       CO934461
VERSION         CO934461.1 GI:51289138
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens

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REFERENCE
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        unpublished (1999)
COMMENT        Contact: Daniela S. Gerhard, Ph.D.
                Office of Cancer Genomics
                National Cancer Institute / NIH
                Bldg. 31 Rm10A07 Bethesda, MD 20892
                Email: c9abbs-remail.nih.gov
                Tissue Procurement: GPCR Consortium
                cDNA Library Preparation: GPCR Consortium
                DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: IRBIS row: c column: 08
                High quality sequence start: 12
                High quality sequence stop: 539.
                Location/Qualifiers

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FEATURES

source

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1..730
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7211818"
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/clone_1lb="NIH_MGC_145"
/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XbaI/XhoI-3', 5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat a Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match      51.1%; Score 517.8; DB 7; Length 730;
Best Local Similarity 91.3%; Pred. No. 2e-98;
Matches 570; Conservative 0; Mismatches 50; Indels 4; Gaps 2;

QY 391 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
DB 688 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
QY 451 CAGCTGACGCTCTGTCAGCGCTGTCAGCGCGGCGCCAGACGAGCGCTGCGCTTCCGC 510
DB 628 CCGC--CTCCCTCGTCAGCGCTTGC--GCCGCGCGGACACGACCTTGCCTTTTCC 573
QY 511 GTCTTACAGCGCGCTTCCAGCGCTTCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 570
DB 572 GTCTTACAGCGCGCTTCCAGCGCTTCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 513
QY 571 ACCTACTCAAGGTGCTCAAGGTGCGCGCTTCAATGCAAGCGCATGCACTGATAC 630
DB 512 ACCTACTCAAGGTGCTCAAGGTGCGCGCTTCAATGCAAGCGCATGCACTGATAC 453
QY 631 ATGCAAGCGTGTGCTGCTGTCGTCAGCTGTCAGCCCGAGTGTGCGGAGCGCTGTGAG 690
DB 452 ATGCAAGCGTGTGCTGCTGTCGTCAGCTGTCAGCCCGAGTGTGCGGAGCGCTGTGAG 393
QY 691 GAGCAGAGCGGAGGAGGAGCAGCGAGCCAGCAAGAAATACAGCACTTCAATAGGAGACCTTC 750
DB 392 GAGCAGAGCGGAGGAGGAGCAGCGAGCCAGCAAGAAATACAGCACTTCAATAGGAGACCTTC 333
QY 751 CTGTGCTGCTGCGCGCTTATGATATCAAGGCTAGTGAAGCTTCTTCCAGGCTGCC 810
DB 332 CTGTGCTGCTGCGCGCTTATGATATCAAGGCTAGTGAAGCTTCTTCCAGGCTGCC 273

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QY	811	ATCGGCTCCACATGGGGGGGGTGTGCTTCAGAGTCTTGCGCTAAGAGAGCGCATCCGAC	870
Db	272	ATGCGCTCCACATGGGGGGGGTGTGCTTCAGAGTCTTGCGCTAAGAGAGCGCATCCGAC	213
QY	871	CCCTTGTGTACTCTCTTACCTGCGACACAGTACCGCAAAAGCTGCAAGGATTTCTGAAC	930
Db	212	CCCTTGTGTACTCTCTTACCTGCGACACAGTACCGCAAAAGCTGCAAGGATTTCTGAAC	153
QY	931	AGGCTTCCTGACACAGACGCTCCATCCATCTCTTGCGCTTCACAGGCGCATCTTCACAGCCAG	990
Db	152	AGGCTTCCTGACACAGACGCTCCATCCATCTCTTGCGCTTCACAGGCGCATCTTCACAGCCAG	93
QY	991	AACATTCTGGCGGCTGTCTGAGTGA	1014
Db	92	AACATTCTGGCGGCTGTCTGAGTGA	69
RESULT 8			
LOCUS	AK042755	1211 bp	mRNA linear HTC 03-APR-2004
DEFINITION			Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730021D22 product:ORPAn G PROTEIN-COUPLE RECEPTOR GPR26 homolog [Rattus norvegicus], full insert sequence.
ACCESSION	AK042755		
VERSION	AK042755.1	GI:26335306	
KEYWORDS	HTC, CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	1	Carninci, P. and Hayashizaki, Y.	
TITLE		High-efficiency full-length cDNA cloning	
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE		99279253	
PUBMED		10349636	
REFERENCE			
AUTHORS	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
TITLE		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)	
MEDLINE		20499374	
PUBMED		11042159	
REFERENCE			
AUTHORS	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitasuna, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaibiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
TITLE		RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer	
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)	
MEDLINE		20530913	
PUBMED		11076861	
REFERENCE			
AUTHORS	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
TITLE		Functional annotation of a full-length mouse cDNA collection	
JOURNAL		Nature 409, 685-690 (2001)	
MEDLINE		11076861	
PUBMED		11076861	
REFERENCE			
AUTHORS	5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
TITLE		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
JOURNAL		Nature 420, 563-573 (2002)	
MEDLINE		6 (bases 1 to 1211)	
PUBMED		12111	
REFERENCE			
AUTHORS	6	Adachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hoti, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,	

	TITLE	Katoch.H., Kawai.J., Kojima.Y., Kondo.S., Komoto.H., Koude.M., Koya.S., Kurihara.C., Matsuyama.T., Miyazaki.A., Murata.M., Nakamura.M., Nishii.K., Nomura.K., Numasaki.R., Ohno.M., Ohsato.N., Okazaki.Y., Saito.R., Saitoh.K., Sakai.C., Sakai.K., Sakazume.N., Sano.H., Sasaki.D., Shibata.K., Shinagawa.A., Shiraki.T., Sogabe.Y., Tagami.M., Tagawa.A., Takahashi.F., Takaku-Akahira.S., Takeda.Y., Tanaka.T., Tomaru.U., Toya.T., Yasunishi.A., Muramatsu.M. and Hayashizaki.Y.
	JOURNAL	Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
	COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/. Location/Qualifiers 1. .1211
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CDS		<1..584 /note="unnamed protein product; ORPHAN G PROTEIN-COUPLED RECEPTOR GPR26 homolog [Rattus norvegicus] (SPRR_090X13, evidence: FASRY, 99.4%ID, 100%length, match=1011) putative" /codon_start=3 /protein_id="BACJ1354.1" /db_xref="GI:26335307" /translation="SWLGFQILVASCTLSGRPDPERLPFAVTSAPFALSFLSLFIVLCFTYLKVAARFHCRIKDVTIMOTLVLDIHHSYVERCLEQRKRROGATKKISIEFFIGFLVCAPAVITRIVELERFSTAPEGMSGVLSCLAYSRAADDPFYSLIRHQYRSCKELINKIPRRSRSHSVGLTGDHSONILPVSE"
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	Matches	526; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
Dy	432	GTCCTGGGTGGGCTGCACCAAGCTGTACGCTTGTCGACGCCGGCGCCAGA 491
Dd	2	GTCCTGGCTGGCTGCACCAAGCTGTATGCTTCGTGCACA CTGGCACGCCGCGCGCGGA 61
Dy	492	CGACGCGCTGGCTGCCTTCCTCACTGGCGCTTCACGCTCTCATGCTTCGCTCTC 551
Dd	62	CGACGCGCTGGCTGCTGCTGTCTTCACCAAGGCTTCACAGCTTCAGCTTCGCTCTC 121
Dy	552	CTTCGTGCTGCTGTGCTGACGTAACCTCAAGGCTTCAGAGTGGCCGCTTCATTGCAA 611
Dd	122	CTTCATGCTGCTGCTGCTTCAAGTACCTCAAGGCTTCAAAGTGGCCGCTTCACACTGCA 181
Dy	612	GCGCATGACGTGATCCATGACAGACGCTGTGTCTGCTGTGTGACCTTGCAACCCAGTGT 671
Dd	182	GCGCATGACGTGTATCCATGACAGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 241
Dy	672	GCGGGAACGCTGTGTGAGAGAGAGAACGCGAGGCGCAACGAGGCAACCAAGAAAGTCAAG 731
Dd	242	GAGGGAACGCTGTGTGAGAGAGAGAACGAGGCGAGCGACAGCGTGCACCAAGAAAGTCAAG 301

Qy	732	TAACCTTCAATAGGAGACCTTTCCTTGTGTGTGGCCCTATATGTGAACACAGGCTATGCGA	791
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Qy	792	GCTCTTCTCAACGATGCCATCGCTCCACATGGGGGGTGTCTTCAAGTGTGGCGTA	851
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Qy	852	CAGCAAGGCGCATTCGACCCCTTTGTGTATCTCTTACTGTGGAGACCGATACCGGAAG	911
Db	422	CAGCAAGGCGCCCTTCTGACCCCTTGTGTATCTCTTCTGGACACCAATACCGAGAG	481
Qy	912	CTGCAGAGGATTTCTGAAAGGGCTCTGCACAGACGCTTCATTCACCTCTTGCGCTAC	971
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Qy	972	AGGCGACTTCAACAGCCAGAACTTCTCCGCGTGTCTAAGCA	1014
Db	542	AGGTGACTTCAACAGCCAGAACTTCTCCAGTGTGGAAATA	584

RESULT 9					
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LOCUS	CB528011	861 bp	mRNA	linear	EST 09-JUL-2003
DEFINITION	UI-M-F10-cfr-1-22-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone				
ACCESSION	IMAGE:6850823 5', mRNA sequence.				
VERSION	CB528011				
KEYWORDS	CB528011.1	GI:29361484			
SOURCE	EST.				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	Mus musculus				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	1 (bases 1 to 861)				
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/ .				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov				
	Tissue Procurement: Dr. Jim Lin, University of Iowa				
	cDNA library preparation: Dr. M. Bento Soares, University of Iowa				
	cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa				
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa				
	Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mouseef1.html				
	This clone was contributed by the Brain Molecular Anatomy Project (BMAP)				
	Seq primer: pYX-5.				

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location/Qualifiers
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Site_2: Not I; The library was constructed according
Donald, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemm Chin, Ph.D.,

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ORIGIN      program coordinator."

Query Match      47.7%; Score 483.4; DB 6; Length 861;
Best Local Similarity 90.5%; Pred. No. 3,4e-91;
Matches 514; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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OY	1	ATGAACCTGTGGAGCGGGGCTGGCGGGGCTACGTGGGGCAGATAGGGTCTGGTG	60
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OY	61	CTGTTCGAACGCGCTGTGTGTCTTGTGCTGTGCACACGCGGAGCATTCGCGCCGACGGCG	120
Db	353	CTGTTCGAACGCGGCTGTGTGTGTCTTGTGCTCTGTGCACACGCGCTGCATCTCGCGCCGACGGCG	412
OY	121	CCGGGGGCTTTCACCCCTGAACCTCAGCGGGGGAAACCTGGCTGTGCACCGTGGTCAACATG	180
Db	413	CCGGGGGCTTTCACCTCTTCACCTCAGCGGTGGAACTGTGTGTACCGTGGTCAACATG	472
OY	181	CCGCTCAACGCTGAGCGGGGCTGTGTGGCGACGCGAGCGCGGGCGAACCGGCTGTGCGCG	240
Db	473	CCACTTACACATCGGCGCGGGCTGTGTGGCACAACGGACGACGCGCGGGGAACCGGCTGTGCGCG	532
OY	241	CTGGCTGTGCTTCTTCGACACCTTCTGGCTGGCCAACTTCATGTCTCAGCATGGCGGCTCT	300
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OY	301	AGCATTCGACCGCTGGGTGGCGGTGTGTCTTCCCGCTGAAGCTACCGGGCCAAATGCGGCTC	360
Db	593	ANCATTCGACCGCTGGGTGGCGGTGTGTGTCTTCCCGCTGAAGCTACCGGTCCAAATGCGGCTC	652
OY	361	CGGCACGCGGGGCTCATGTGTGGCCMACACGTTGGGTGCACGCGGCTCACTTCCACAGCGCC	420
Db	653	CGAATGTGCGGCTTTCATGTGTGGCCMACACGTGGGTGCACGCGGCTCACTTTCGCGGCAC	712
OY	421	GGCGTCCGCTGTGTCTGTGGCTCGGCTTCCACACAGCTGTACCGGCTCTGTGCACGCTGTGCAGC	480
Db	713	GGCGTCCGCTGTGTCTGTGGCTCGGCTTCCACACAGCTATATGCTGTGTGCACACTGTGTGCAGC	772
OY	481	CGGCGGCCAGACGACGCGCTGCGGCTTGGCGGCTTTCACACTGGCGGCTTTCACAGCTTTCAGC	540
Db	773	CGGCGGCCAGACGACGCGCTGCGGCTTGGCGGCTTTCACACTGGCGGCTTTCACAGCTTTCAGC	832
OY	541	TTTCTGTCTTCTTCTGTGTGTGTCTGTGCT	568
Db	833	TTTCTGTCTTCTTCTGTGTGTGTGTGTGCTGTGCT	860

RESULT 10
LOCUS BB639955
DEFINITION BB639955 RIKEN full-length enriched, 7 day neonate cerebellum Mus musculus cDNA A730021D22 5', mRNA sequence.
ACCESSION BB639955
VERSION BB639955.1 GI:15401479
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 703)
AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanaigaki, T., Hara, A., Hizumoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, U., Komuro, H., Kouda, M., Koya, S., Matuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
unpublished (2001)
TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
JOURNAL
COMMENT Contact: Yoshinhide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	ATGAACCTCGGAGACGCGGGCTGAGCGGGCTACTGGTGGGACGATGGCGCTCTGCTG	60	
DB	1	ATGAACCTCGGAGACGCGGGCTGAGCGGGCTACTGGTGGGACGATGGCGCTCTGCTG	60	
QY	61	CTGTCCACGCGGTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120	
DB	61	CTGTCCACGCGGTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120	
QY	121	CGGCGCTCTTCAACCTGAACTCAGTGGGGAACCTGCTGGGACCGGTGCAACATG	180	
DB	121	CGGCGCTCTTCAACCTGAACTCAGTGGGGAACCTGCTGGGACCGGTGCAACATG	180	
QY	181	CGGCTACGCTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240	
DB	181	CGGCTACGCTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240	
QY	241	CTGGCTGCTCTTCTGCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300	
DB	241	CTGGCTGCTCTTCTGCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300	
QY	301	AGGATGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360	
DB	301	AGGATGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360	
QY	361	CGGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420	
DB	361	CGGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420	
QY	421	GGCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480	
DB	421	GGCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480	
QY	481	CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540	
DB	481	CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540	
QY	541	TTCCGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600	
DB	541	TTCCGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600	
QY	601	TTCCATTGCAAGCGCATCGAAGTATCAGATGAGACGCTGCTGCTGCTGCTGCTGCTG	660	
DB	601	TTCCATTGCAAGCGCATCGAAGTATCAGATGAGACGCTGCTGCTGCTGCTGCTGCTG	660	
QY	661	CACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720	
DB	661	CACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720	
QY	721	AGGATGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780	
DB	721	AGGATGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780	
QY	781	AGGCTAGTGAAGCTCTTCTGCAAGTGTCCATCGGCTTCCATGAGGAGTGTCTGCAAG	840	
DB	781	AGGCTAGTGAAGCTCTTCTGCAAGTGTCCATCGGCTTCCATGAGGAGTGTCTGCAAG	840	
QY	841	TGCTTGGCTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900	
DB	841	TGCTTGGCTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900	
QY	901	TACCGCAAAAGCTGCAAGAGATTTCTGAACAGGCTCTGCAAGAGCTTCCATCACTCC	960	
DB	901	TACCGCAAAAGCTGCAAGAGATTTCTGAACAGGCTCTGCAAGAGCTTCCATCACTCC	960	
QY	961	TTCTGCTTCAAGCGCATCTCAAGCAAGAACATTTGCGGAGTGTGATGA 1014		
DB	961	TTCTGCTTCAAGCGCATCTCAAGCAAGAACATTTGCGGAGTGTGATGA 1014		

RESULT 2
US-10-735-991-1

; Sequence 1, Application US/10735991				
; Publication No. US20040121395A1				
; GENERAL INFORMATION:				
; APPLICANT: GOODNOW, Jr., Robert Alan				
; APPLICANT: MARK, David Fu-Chi				
; APPLICANT: MARTIN, Mitchell Lee				
; APPLICANT: ROSINSKI, James Andrew				
; TITLE OF INVENTION: Sequence #115 as a target for identifying weight modulating				
; FILE REFERENCE: 21366				
; CURRENT APPLICATION NUMBER: US/10/735,991				
; PRIOR FILING DATE: 2003-12-15				
; PRIOR FILING DATE: 2002-12-23				
; NUMBER OF SEQ ID NOS: 6				
; SOFTWARE: PatentIn version 3.2				
; SEQ ID NO 1				
; LENGTH: 1011				
; TYPE: DNA				
; ORGANISM: Mus musculus				
; FEATURE:				
; NAME/KEY: GPCR #115				
; LOCATION: (1)-(1011)				
; OTHER INFORMATION: CHR7-36867				
US-10-735-991-1				
Query Match 99.7%; Score 1011; DB 19; Length 1011;				
Best Local Similarity 100.0%; Pred. No. 1,6e-252;				
Matches 1011; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	ATGAACCTCGGAGACGCGGGCTGAGCGGGCTACTGGTGGGACGATGGCGCTCTGCTG	60	
DB	1	ATGAACCTCGGAGACGCGGGCTGAGCGGGCTACTGGTGGGACGATGGCGCTCTGCTG	60	
QY	61	CTGTCCACGCGGTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120	
DB	61	CTGTCCACGCGGTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120	
QY	121	CGGCGCTCTTCAACCTGAACTCAGTGGGGAACCTGCTGGGACCGGTGCAACATG	180	
DB	121	CGGCGCTCTTCAACCTGAACTCAGTGGGGAACCTGCTGGGACCGGTGCAACATG	180	
QY	181	CGGCTACGCTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240	
DB	181	CGGCTACGCTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240	
QY	241	CTGGCTGCTCTTCTGCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300	
DB	241	CTGGCTGCTCTTCTGCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300	
QY	301	AGGATGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360	
DB	301	AGGATGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360	
QY	361	CGGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420	
DB	361	CGGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420	
QY	421	GGCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480	
DB	421	GGCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480	
QY	481	CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540	
DB	481	CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540	
QY	541	TTCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600	
DB	541	TTCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600	
QY	601	TTCCATTGCAAGCGCATCGAAGTATCAGATGAGACGCTGCTGCTGCTGCTGCTGCTG	660	
DB	601	TTCCATTGCAAGCGCATCGAAGTATCAGATGAGACGCTGCTGCTGCTGCTGCTGCTG	660	

QY 661 CACCCAGTGTGGGAAACGCTGTCTGAGAGCAAGAGCGGAGCGACAGCGACCAACC 720
DB 661 CACCCAGTGTGGGAAACGCTGTCTGAGAGCAAGAGCGGAGCGACAGCGACCAACC 720
QY 721 AAGAGATGAGCAGCTTCTATGAGGACCTTCTGTGTGTCTTGGGCGGCTTATGATACCC 780
DB 721 AAGAGATGAGCAGCTTCTATGAGGACCTTCTGTGTGTCTTGGGCGGCTTATGATACCC 780
QY 781 AGGCTAGTGAAGCTTCTTCCAGCGGTGCCATCGGCTCCCACTGGGAGGTGTCTCCAG 840
DB 781 AGGCTAGTGAAGCTTCTTCCAGCGGTGCCATCGGCTCCCACTGGGAGGTGTCTCCAG 840
QY 841 TGCTTGGCGTACAGCAAGCGCGCATCCGACCCCTTGTGTACTCTTACTGCGACACAG 900
DB 841 TGCTTGGCGTACAGCAAGCGCGCATCCGACCCCTTGTGTACTCTTACTGCGACACAG 900
QY 901 TACCGCAAAAGCTGCAAGAGATTTCTGAACAGGCTCTGCAACAGCTCATCATCTCC 960
DB 901 TACCGCAAAAGCTGCAAGAGATTTCTGAACAGGCTCTGCAACAGCTCATCATCTCC 960
QY 961 TCTGCGCTCACAGCGCACTCTCACAGCGCAACATTTGCGCGGTGTCTAG 1011
DB 961 TCTGCGCTCACAGCGCACTCTCACAGCGCAACATTTGCGCGGTGTCTAG 1011

RESULT 3
US-10-757-262-129
; Sequence 129, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16652, 1587, 22073, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32820, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 2115, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MP103-007PLNOMNIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 2530
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (186)...(1199)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2530)
; OTHER INFORMATION: n = A,T,C or G
US-10-757-262-129
Query Match 99.5%; Score 1009.2; DB 19; Length 2530;
Best Local Similarity 99.7%; Pred. No. 4.9e-252;
Matches 1011; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAATCTGTGAGACGCGGCGCTGCGGCGCTACTGTGTGAGCAAGATGGCGTCTGCTG 60
DB 186 ATGAATCTGTGAGACGCGGCGCTGCGGCGCTACTGTGTGAGCAAGATGGCGTCTGCTG 245
QY 61 CTGTCCAGCGCGTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 120
DB 246 CTGTCCAGCGCGTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 305
QY 121 CCGGCGCTCTTCAACCTGAACCTCACTGTGAGGAACTGTGTGTGTGTGTGTGTGTGTGTGT 180
DB 306 CCGGCGCTCTTCAACCTGAACCTCACTGTGAGGAACTGTGTGTGTGTGTGTGTGTGTGTGT 365
QY 181 CCGCTCACGCTGTGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 366 CCGCTCACGCTGTGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 425
QY 241 CTGCTGCTCTTCTGTCAACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 426 CTGCTGCTCTTCTGTCAACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 485
QY 301 AGCATGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 486 AGCATGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 545
QY 361 CCGGAGCGGCGGCTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 546 CCGGAGCGGCGGCTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 605
QY 421 GCGCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB 606 GCGCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 665
QY 481 CCGCGGCGCAAGCGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 666 CCGCGGCGCAAGCGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 725
QY 541 TTCCTGCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 726 TTCCTGCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 785
QY 601 TTCATTTGCAAGCGCATGCACTGATCACCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 786 TTCATTTGCAAGCGCATGCACTGATCACCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 845
QY 661 CACCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 846 CACCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 905
QY 721 AAGAGATGAGCAGCTTCTATGAGGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 906 AAGAGATGAGCAGCTTCTATGAGGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 965
QY 781 AGGCTAGTGAAGCTTCTTCCAGCGGTGCCATCGCTCCCACTGGGAGGTGTCTGTCTCAAG 840
DB 966 AGGCTAGTGAAGCTTCTTCCAGCGGTGCCATCGCTCCCACTGGGAGGTGTCTGTCTCAAG 1025
QY 841 TGCTTGGCGTACAGCAAGCGCGCATCCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 1026 TGCTTGGCGTACAGCAAGCGCGCATCCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1085

QY 901 TACCGAAAAAGCTGACAGAGATTCTGAACAGGCTCTGACAGACGCTCCATCCACTCC 960
DB 1086 TACCGAAAAAGCTGACAGAGATTCTGAACAGGCTCTGACAGACGCTCCATCCACTCC 1145
QY 961 TCTGGCTTCACAGGCACTCTCACAGCCAGAACATTTCGCCGTGTGTGATA 1014
DB 1146 TCTGGCTTCACAGGCACTCTCACAGCCAGAACATTTCGCCGTGTGTGATA 1199

RESULT 4
US-09-742-732-1
Sequence 1, Application US/09742732
Patent No. US20020055137A1
GENERAL INFORMATION:
APPLICANT: M. Alexandra Glucksmann and Keith Robison
TITLE OF INVENTION: LIGAND RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/742,732
FILING DATE: 20-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/175,983
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 184..1194
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-742-732-1

Query Match 99.5%; Score 1009.2; DB 9; Length 2581;
Best Local Similarity 99.7%; Pred. No. 4.9e-252;
Matches 1011; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAAGTCTGGGAGCGGCGCTGAGCGGCTGCTGAGGAGCAAGATGGGCTCTGCTG 60
DB 184 ATGAAGTCTGGGAGCGGCGCTGAGCGGCTGCTGAGGAGCAAGATGGGCTCTGCTG 243
QY 61 CTGTCCAAAGCGGCTGTGTCTCTGCTGCTGCTGCAACAGCGGCAATCCGCCGAGGCG 120
DB 244 CTGTCCAAAGCGGCTGTGTCTCTGCTGCTGCTGCAACAGCGGCAATCCGCCGAGGCG 303
QY 121 CCGGCGCTTCACCGTGAACCTCAAGTGCAGGAACTGCTGTGCAACCGTGTGTAATG 180
DB 304 CCGGCGCTTCACCGTGAACCTCAAGTGCAGGAACTGCTGTGCAACCGTGTGTAATG 363
QY 181 CCGCTACGCTGCGCGGCTGTGTGCGAGCGGAGCCGCGGAGACCGGCTGTGCGCG 240

DB 364 CCGCTACGCTGCGCGGCTGTGTGCGAGCGGAGCTCGCGGAGCAACCGCTGTGCGCG 423
QY 241 CTGGCTGCTCTCTGACACCTTCTGAGTGCACATCCATGCTGACAGATGGCGGCGCTC 300
DB 424 CTGGCTGCTCTCTGACACCTTCTGAGTGCACATCCATGCTGACAGATGGCGGCGCTC 483
QY 301 AGCATGACCGCTGTGGTGGCGGTGTGTCTTCGCGTGAAGCTACCGGCGCAAGATCGGCTC 360
DB 484 AGCATGACCGCTGTGGTGGCGGTGTGTCTTCGCGTGAAGCTACCGGCGCAAGATCGGCTC 543
QY 361 CCGAGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 544 CCGAGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 603
QY 421 GCGCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB 604 GCGCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 663
QY 481 CCGCGCGCAAGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 664 CCGCGCGCAAGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 723
QY 541 TTCTGCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 724 TTCTGCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 783
QY 601 TTCCATTGCAAGGCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 660
DB 784 TTCCATTGCAAGGCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 843
QY 661 CACCCAGTGTGGGAGACGCTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 844 CACCCAGTGTGGGAGACGCTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
QY 721 AAGAAGTACGACCTTTCATAGGAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 904 AAGAAGTACGACCTTTCATAGGAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 963
QY 781 AGGCTAGTGAAGCTTCTTCACGAGTGCATCGGCTCCAGTGGGAGGAGTGTGTGTGTGT 840
DB 964 AGGCTAGTGAAGCTTCTTCACGAGTGCATCGGCTCCAGTGGGAGGAGTGTGTGTGTGT 1023
QY 841 TGCTTGGCTGACAGAGCGCGCATCGACCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 1024 TGCTTGGCTGACAGAGCGCGCATCGACCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1083
QY 901 TACCGAAAAAGCTGACAGAGATTCTGAACAGGCTCTGACAGACGCTCCATCCACTCC 960
DB 1084 TACCGAAAAAGCTGACAGAGATTCTGAACAGGCTCTGACAGACGCTCCATCCACTCC 1143
QY 961 TCTGGCTTCACAGGCACTCTCACAGCCAGAACATTTCGCCGTGTGTGATA 1014
DB 1144 TCTGGCTTCACAGGCACTCTCACAGCCAGAACATTTCGCCGTGTGTGATA 1197

RESULT 5
US-10-921-613-1
Sequence 1, Application US/10921613
Publication No. US20050079550A1
GENERAL INFORMATION:
APPLICANT: M. Alexandra Glucksmann and Keith Robison
TITLE OF INVENTION: LIGAND RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

Db 241 CTGGCTGCTTCTCTGACACCTTCTGGCTGCAATCTCATGCTCAGATGAGCCGCTC 300
Qy 301 AGCATGCAACCGCTGGGTGGCGGTGCTCTTCCGCTGAGCTACCGGGCCAAATGCGCTC 360
Db 301 AGCATGCAACCGCTGGGTGGCGGTGCTCTTCCGCTGAGCTACCGGGCCAAATGCGCTC 360
Qy 361 CGGACCGGGGCTCATGTGGCTTACACAGTGGCTGACAGGGCTCACTTCCAGCCGCC 420
Db 361 CGGACCGGGGCTCATGTGGCTTACACAGTGGCTGACAGGGCTCACTTCCAGCCGCC 420
Qy 421 GCGCTGCGCTTCTGCTGGCTGGCTTCCACAGCTGTAAGCTGTGACAGCTGAGC 480
Db 421 GCGCTGCGCTTCTGCTGGCTGGCTTCCACAGCTGTAAGCTGTGACAGCTGAGC 480
Qy 481 CGGCGCGGACGACGAGCGCTGCTTCCGCTTCTCACTGGCGCTTCAAGCTTCTAGC 540
Db 481 CGGCGCGGACGACGAGCGCTGCTTCCGCTTCTCACTGGCGCTTCAAGCTTCTAGC 540
Qy 541 TTCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TTCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 661 CACCCAGTGTGCGGGAACGCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 CACCCAGTGTGCGGGAACGCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 AAGAAATCAGACCTTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 AAGAAATCAGACCTTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 781 AGGCTAGTGAAGCTTCTTCTCAAGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 AGGCTAGTGAAGCTTCTTCTCAAGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 841 TGCTTGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 TGCTTGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 901 TACCGAAAAGCTGCAAGAGATTCTGAAAGAGCTCTGCAAGAGCTGCAATCAGCTCC 960
Db 901 TACCGAAAAGCTGCAAGAGATTCTGAAAGAGCTCTGCAAGAGCTGCAATCAGCTCC 960
Qy 961 TCTGGCTCAGAGGCGACTCTCAGAGCGAAGAACTTCTGCGGTGTCTGAG 1011
Db 961 TCTGGCTCAGAGGCGACTCTCAGAGCGAAGAACTTCTGCGGTGTCTGAG 1011

RESULT 8

US-10-505-486-172
; Sequence 172, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILER REFERENCE: P03-0006CT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 172
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Human
US-10-505-486-172

Query Match 99.2%; Score 1006.2; DB 21; Length 1728;
Best Local Similarity 99.7%; Pred. No. 2,9e-251;
Matches 1008; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAATCTGTGGAGACCGGCGCTGAGCGGCTGATGCTGGGACAGATGGCGTCTGCTG 60
Db 1 ATGAATCTGTGGAGACCGGCGCTGAGCGGCTGATGCTGGGACAGATGGCGTCTGCTG 60
Qy 61 CTGTCCAAACGCGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61 CTGTCCAAACGCGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 121 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGGAACCTGTGTGCAACGCTGTCAATG 180
Db 121 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGGAACCTGTGTGCAACGCTGTCAATG 180
Qy 181 CCGCTACGCTGCGCGGCTGTGAGCGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 181 CCGCTACGCTGCGCGGCTGTGAGCGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG 240
Qy 241 CTGGCTGCTTCTCTGCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 CTGGCTGCTTCTCTGCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 301 AGCATGACCGCTGGGTGGCGGTGCTTCCGCTGAGCTACCGGGCCAAATGCGCTC 360
Db 301 AGCATGACCGCTGGGTGGCGGTGCTTCCGCTGAGCTACCGGGCCAAATGCGCTC 360
Qy 361 CGGACCGGGGCTCATGTGGCTTACACAGTGGCTGACAGGGCTCACTTCCAGCCGCC 420
Db 361 CGGACCGGGGCTCATGTGGCTTACACAGTGGCTGACAGGGCTCACTTCCAGCCGCC 420
Qy 421 GCGCTGCGCTTCTGCTGGCTGGCTTCCACAGCTGTAAGCTGTGAGAGCTGTGAGC 480
Db 421 GCGCTGCGCTTCTGCTGGCTGGCTTCCACAGCTGTAAGCTGTGAGAGCTGTGAGC 480
Qy 481 GCGCTGCGCTTCTGCTGGCTGGCTTCCACAGCTGTAAGCTGTGAGAGCTGTGAGC 480
Db 481 GCGCTGCGCTTCTGCTGGCTGGCTTCCACAGCTGTAAGCTGTGAGAGCTGTGAGC 480
Qy 481 GCGGCGGACAGAGAGCGCTGCGCTTCCGCTTCTCACTGAGCGCTTCCAGCGCTCAGC 540
Db 481 GCGGCGGACAGAGAGCGCTGCGCTTCCGCTTCTCACTGAGCGCTTCCAGCGCTCAGC 540
Qy 541 TTCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TTCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 661 CACCCAGTGTGCGGGAACGCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 CACCCAGTGTGCGGGAACGCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 AAGAAATCAGACCTTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 AAGAAATCAGACCTTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 781 AGGCTAGTGAAGCTTCTTCTCAAGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 AGGCTAGTGAAGCTTCTTCTCAAGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 841 TGCTTGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 TGCTTGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 901 TACCGAAAAGCTGCAAGAGATTCTGAAAGAGCTCTGCAAGAGCTGCAATCAGCTCC 960
Db 901 TACCGAAAAGCTGCAAGAGATTCTGAAAGAGCTCTGCAAGAGCTGCAATCAGCTCC 960
Qy 961 TCTGGCTCAGAGGCGACTCTCAGAGCGAAGAACTTCTGCGGTGTCTGAG 1011
Db 961 TCTGGCTCAGAGGCGACTCTCAGAGCGAAGAACTTCTGCGGTGTCTGAG 1011

RESULT 9
US-10-083-168-97
; Sequence 97, Application US/10083168
; Publication No. US2003023069A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Maciejewski-Lemlor, Dominique
; APPLICANT: Leonard, James N.
; APPLICANT: Ortuno, Daniel
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Endogenous And No. US2003023069A1-Endogenous, Constitutively Act
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0320
; CURRENT APPLICATION NUMBER: US/10/083,168
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent version 3.1
; SEQ ID NO 97
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-083-168-97

Query Match 97.3%; Score 986.8; DB 14; Length 1014;
Best Local Similarity 98.3%; Pred. No. 3e-246;
Matches 997; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 ATGAATCTGTGGAGACGGGGCTTGGAGGCTACTGTGGACAGATGGGCTGTGCTG 60
DB 1 ATGAATCTGTGGAGACGGGGCTTGGAGGCTACTGTGGACAGATGGGCTGTGCTG 60
QY 61 CTGTCCAAAGCGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 120
DB 61 CTGTCCAAAGCGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 120
QY 121 CCGGGGCTTCAACCTGAACTCAAGTGGGGAACTGCTGTGTCAACCGTGTGTCAATG 180
DB 121 CCGGGGCTTCAACCTGAACTCAAGTGGGGAACTGCTGTGTCAACCGTGTGTCAATG 180
QY 121 CCGGGGCTTCAACCTGAACTCAAGTGGGGAACTGCTGTGTCAACCGTGTGTCAATG 180
DB 121 CCGGGGCTTCAACCTGAACTCAAGTGGGGAACTGCTGTGTCAACCGTGTGTCAATG 180
QY 181 CCGGCTACGCTGTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 240
DB 181 CCGGCTACGCTGTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 240
QY 241 CTGGCTGTCTTCTTCTGTGAACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 300
DB 241 CTGGCTGTCTTCTTCTGTGAACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 300
QY 301 AGCATTCGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 360
DB 301 AGCATTCGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 360
QY 361 CCGGACGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 420
DB 361 CCGGACGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 420
QY 421 GCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 480
DB 421 GCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 480
QY 481 CCGGGGCGGACGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 540
DB 481 CCGGGGCGGACGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 540
QY 541 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 600
DB 541 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 600
QY 601 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 660
DB 601 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 660

QY 661 CACCCAGTGTGGGAGACGCTGTCTGTGAAGACAGACCGAGGCGACAGGCGCCACC 720
DB 661 CACCCAGTGTGGGAGACGCTGTCTGTGAAGACAGACCGAGGCGAGGCGAGGCGCCACC 720
QY 721 AAGAATGACGACCTTCTATAGGAGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTG 780
DB 721 AAGAATGACGACCTTCTATAGGAGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTG 780
QY 781 AGGCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 840
DB 781 AGGCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 840
QY 841 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 900
DB 841 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 900
QY 901 TACCGGAAAGCTGTGAAGAGATTCTGAAACAGGCTGTGTGTGTGTGTGTGTGTGTG 960
DB 901 TACCGGAAAGCTGTGAAGAGATTCTGAAACAGGCTGTGTGTGTGTGTGTGTGTGTG 960
QY 961 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1014
DB 961 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1014

RESULT 10
US-10-735-991-3
; Sequence 3, Application US/10735991
; Publication No. US20040121395A1
; GENERAL INFORMATION:
; APPLICANT: GOODNOW, Jr., Robert Alan
; APPLICANT: MARK, David Fu-Chi
; APPLICANT: MARTIN, Mitchell Lee
; APPLICANT: ROSINSKI, James Andrew
; TITLE OF INVENTION: Sequence #115 as a target for identifying weight modulating
; FILE REFERENCE: 21366
; CURRENT APPLICATION NUMBER: US/10/735,991
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/436,375
; PRIOR FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent version 3.2
; SEQ ID NO 3
; LENGTH: 1172
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: GPCR #115
; LOCATION: (1)..(1172)
; OTHER INFORMATION: O9QX13
US-10-735-991-3

Query Match 85.6%; Score 868.4; DB 19; Length 1172;
Best Local Similarity 91.0%; Pred. No. 1.ee-215;
Matches 923; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1 ATGAATCTGTGGAGACGGGGCTTGGAGGCTACTGTGGACAGATGGGCTGTGCTG 60
DB 27 ATGAATCTGTGGAGACGGGGCTTGGAGGCTACTGTGGACAGATGGGCTGTGCTG 86
QY 61 CTGTCCAAAGCGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 120
DB 87 CTGTCCAAAGCGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 146
QY 121 CCGGGGCTTCAACCTGAACTCAAGTGGGGAACTGCTGTGTGTGTGTGTGTGTGTGTG 180
DB 147 CCGGGGCTTCAACCTGAACTCAAGTGGGGAACTGCTGTGTGTGTGTGTGTGTGTGTG 206
QY 181 CCGGCTACGCTGTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 240
DB 207 CCGGCTACGCTGTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 266


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? PRIOR FILING DATE: 1999-12-23
? PRIOR APPLICATION NUMBER: 60/181,749
? PRIOR FILING DATE: 2000-02-11
? Remaining Prior Application data removed - See File Wrapper or PAMM
? NUMBER OF SEQ ID NOS: 133
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 1
?
? LENGTH: 1092
?
? TYPE: DNA
? ORGANISM: Homo sapiens
?
? US-10-321-807-31

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[illegible]

Db 841 TGCGTACCTACAGCAGAGGCGGTGCGCCAGCCGGTTCAGAGTACTGTGCTCCGCGGCGCG 900
 Oy 901 TACCGGAAAGCTGCAAGAGATTCTGAACAGGCTCTCGACAGAGCTCTCATCCACTCC 960
 Db 901 TTCCGCGAAGTCTCTGCGCGGCGATGTGACACGGCTGTGAAGAGAACCCGCGCCACGCA 960
 Oy 961 TCTGACC 967
 Db 961 TTCACCC 967

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RESULT 13
US-10-321-807-31
; Sequence 31, Application US/10321807
; Publication NO. US20040137563A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-321-807-31

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[illegible]

Oy	241	CTGGGCGCTTCTCTGCACACCTTCCGTGGCTGGCAACCTCAATGCTCAAGATAGGCGGGCTC	300
Oy	241	CTGGGCGCTTCTCTGCACACCTTCCGTGGCTGGCAACCTCAATGCTCAAGATAGGCGGGCTC	300
Db	241	GTCAATTGGGCTTCTTGACACCTTCTCGGGCTTCACAGCGGGCGCTGAGCGTGGCGGGCTG	300
Oy	301	AGCATCGACCGCTGGGTGGCCGTGATCTTCCGCTGAGCTACCGGGCCAAAGATGCGCTTC	360
Db	301	AGCGAGAACCAAGTGGCTGGCAATGGGGCTTCCACTGGCTAAGCCCGAGCGCTTGCACCG	360
Oy	361	CGCGAGCGGGCGCTATGATGGCTTACAGTGGCTGACGGCTCACTTCCTCCAGCGGC	420
Db	361	CGCTATGCGGGCTGCTGCTGGGCTGTGGCTGGGGACAGTGGCTGGCTTCTCAGCGGCT	420
Oy	421	GGGCTGGCCCTGATCCCTGGGCTCGGCTTCCACAGCTGTAGCCCTCGTGCACCGCTGTACAG	480
Db	421	GGACTTGGGTGCTCGTGGCTTGGCTTACAGAGCGCCTTGGCGTCTGTGTGCTGGCGCTG	480
Oy	481	CGGCGGGCCAGACGAGCGCTGGGCTTGGCGCTTTCATCTGAGCGCCTTCCACGCTTCAGC	540
Db	481	CGGCGCGAGCTGAGGGGTCCGGCTTCCAGGCTTACCGCCACGCTTCATAGCGGTGGG	540
Oy	541	TTCCTGCTCTCCTTGGTGGTGGCTCTGCTGACGTAAGTCTCAAGGTCTCAAGGTGGCCCG	600
Db	541	TTCGTGCTGCGCCCTGGCGGTGGCTGTGCTGCTACCTCGCTCCAGGTGACCGGGTGGACGC	600
Oy	601	TTCGCAATGGCAAGGCAATCGAGTATCACATGACACAGCTGGTGGCTGGCTGTGGACCTG	660
Db	601	AGCCACTGCAACGATGAGACCCGTACCATATGAAAGGCTGGCGTGGCTGGCGCACTTG	660
Oy	661	CACCCCAAGTGTGGGGAAAGCTGTCTGTGAGAGACAAACGAGAGCGACAGCGAGCCACC	720
Db	661	CACCCCAAGTGTGGGGAAAGCTGTCTGTGAGAGACAAACGAGAGCGAGCGAGCCACC	720
Oy	721	AAGAAATCAGACCTTCATAGAGAACTTCTTGTGTGCTTCCGCGCTTATGTGATCACC	780
Db	721	AGGAAGATTGGCATTTGCTATTGCAACTTCTTCATCTGTGCTTGGCCCGATATGATAGCC	780
Oy	781	AGGCTAGTGGAACTTCTTCTCCACGGTGGCCCATTCGCTCCCATGGGGGGTGTCTGCAG	840
Db	781	AGGCTAGTGGAACTTCTTCTCCACGGTGGCCCATTCGCTCCCATGGGGGGTGTCTGCAG	840
Oy	841	TGCTTGGCGTACAGCAAGGCGCGCATTCGACCCCTTGTGTGATCTCTTATCTGGCAGACAG	900
Db	841	TGCTTGGCGTACAGCAAGGCGCGCATTCGACCCCTTGTGTGATCTCTTATCTGGCAGACAG	900
Oy	901	TACGCGAAAAGCTGCAGAGGAGATTCTGAACAGGCTCTTGCACAGACGCTTCATTCACCTCC	960
Db	901	TTCGCGCAAGTCTCGGCGCGGATGATGGTGCACCGGCTCTGAAGAGAACCCCGGCGCCAGCA	960
Oy	961	TCTGGGC 967	
Db	961	TTCACCC 967	

RESULT 14
 US-10-314-048A-31
 : Sequence 31, Application US/10314048A
 : Publication No. US20040142372A1
 : GENERAL INFORMATION:
 : APPLICANT: Unett, David J.
 : APPLICANT: Chen, Ruoping
 : APPLICANT: Richman, Jeremy
 : APPLICANT: Connolly, Daniel
 : APPLICANT: Dang, Huang T.
 : APPLICANT: Choi, Bryan
 : APPLICANT: Leonard, James
 : APPLICANT: Hakak, Yaron
 : APPLICANT: Liaw, Chen
 : APPLICANT: Lowitz, Kevin P.
 : APPLICANT: Behan, Dominic P.
 : APPLICANT: Chalmers, Derek T.
 : APPLICANT: Lerner, Michael
 : TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof

```

; TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
; FILE REFERENCE: 22-us6.cip
; CURRENT APPLICATION NUMBER: US/10/314,048A
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: SeqId version 3.1
; SEQ ID NO 31
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-314-048A-31

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[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 12:50:16 ; Search time 210 Seconds
(without alignments)
7900.879 Million cell updates/sec

Title: US-10-735-991-5

Perfect score: 1014
Sequence: 1 atgaactcgtgagcgcgsg9.....ctctgcggtgtctgagtga 1014

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
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2: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1009.2	99.5	2581	2	US-09-013-634-1
2	1006.2	99.2	1011	2	US-09-013-634-3
3	79.2	7.8	1047	3	US-08-540-6508-6
4	79.2	7.8	1050	4	US-09-826-509-502
5	79.2	7.8	1053	4	US-09-016-434-1423
6	79.2	7.8	1110	3	US-08-513-8748-31
7	79.2	7.8	1110	3	US-08-776-971-26
8	79.2	7.8	1110	4	US-09-461-4368-31
9	79.2	7.8	1110	4	US-09-576-290-26
10	79.2	7.8	1331	3	US-08-513-9748-322
11	79.2	7.8	1331	3	US-08-776-971-103
12	79.2	7.8	1331	4	US-09-576-290-103
13	79.2	7.8	1882	3	US-08-540-6508-11
14	79.2	7.8	1033	3	US-08-693-308-1
15	73.8	7.3	1335	2	US-08-985-090-3
16	73.8	7.3	1335	3	US-09-165-543-3
17	73.8	7.3	1335	3	US-09-167-354-6
18	73.8	7.3	1335	3	US-09-642-855-6
19	73.8	7.3	1335	3	US-09-642-855-6
20	73.8	7.3	2050	4	US-09-642-514-6
21	73.8	7.3	2655	4	US-09-891-053-21
22	73.8	7.3	2659	2	US-08-985-090-1
23	73.8	7.3	2659	3	US-09-165-543-1
24	73.8	7.3	2659	3	US-09-167-354-5
25	73.8	7.3	2659	3	US-09-642-855-5
26	73.8	7.3	2659	3	US-09-642-855-5
27	73.6	7.3	1161	1	US-08-086-439C-2

28	73.6	7.3	1161	1	US-08-434-877-2	Sequence 2, Appl1
29	73.6	7.3	1367	3	US-08-475-742-3	Sequence 3, Appl1
30	73.6	7.3	1367	3	US-08-261-293-3	Sequence 3, Appl1
31	73.6	7.3	1504	4	US-09-016-434-1276	Sequence 1276, Ap
32	72	7.1	1370	1	US-08-056-051-1	Sequence 1, Appl1
33	72	7.1	1370	1	US-07-928-611-17	Sequence 17, Appl1
34	72	7.1	1370	2	US-08-487-811A-17	Sequence 17, Appl1
35	72	7.1	1370	3	US-09-060-694-17	Sequence 17, Appl1
36	72	7.1	1370	3	US-09-378-074-17	Sequence 17, Appl1
37	72	7.1	1370	5	PCT-US93-07370-17	Sequence 17, Appl1
38	72	7.1	1466	1	US-08-056-051-3	Sequence 3, Appl1
39	72	7.1	1466	2	US-07-928-611-19	Sequence 19, Appl1
40	72	7.1	1466	2	US-08-487-811A-19	Sequence 19, Appl1
41	72	7.1	1466	3	US-09-060-694-19	Sequence 19, Appl1
42	72	7.1	1466	3	US-09-378-074-19	Sequence 19, Appl1
43	72	7.1	1466	5	PCT-US93-07370-19	Sequence 19, Appl1
44	72	7.1	1610	1	US-08-056-051-5	Sequence 5, Appl1
45	72	7.1	1610	1	US-07-928-611-21	Sequence 21, Appl1

ALIGNMENTS

RESULT 1
US-09-013-634-1
Sequence 1, Application US/09013634
Patent No. 5945307
GENERAL INFORMATION:
APPLICANT: M. Alexandra Glucksmann and Keith Robinson
TITLE OF INVENTION: LIGAND RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,634
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 184..1194
US-09-013-634-1
Query Match 99.5%, Score 1009.2, DB 2, Length 2581,
Best Local Similarity 99.7%, Pred. No. 36-205,
Matches 1011, Conservative 0, Mismatches 3, Indels 0, Gaps 0;

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QY 1 ATGAACCTGCGGAGCGCGGCGCTGAGTGGGCAACGATGGGCGTCTGCTG 60
DB 184 ATGAACCTGCGGAGCGCGGCGCTGAGTGGGCAACGATGGGCGTCTGCTG 243
QY 61 CTGTCCAAAGCGGCGGCGCTGAGTGGGCAACGATGGGCGTCTGCTG 120
DB 244 CTGTCCAAAGCGGCGGCGCTGAGTGGGCAACGATGGGCGTCTGCTG 303
QY 121 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 180
DB 304 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 363
QY 181 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 240
DB 364 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 423
QY 241 CTGGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 300
DB 424 CTGGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 483
QY 301 AGCATGACCGGCGGCGCTGAGTGGGCAACCTGCTGCAACGCTGCAATG 360
DB 484 AGCATGACCGGCGGCGCTGAGTGGGCAACCTGCTGCAACGCTGCAATG 543
QY 361 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 420
DB 544 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 603
QY 421 GCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 480
DB 604 GCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 663
QY 481 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 540
DB 664 CCGGCGCTCTTCAACCTGAACTTCAAGTGGGCAACCTGCTGCAACGCTGCAATG 723
QY 541 TTCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 724 TTCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
QY 601 TTCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 784 TTCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
QY 661 CACCCGAGTGTGCGGAGCGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
DB 844 CACCCGAGTGTGCGGAGCGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 903
QY 721 AAGAAATCAGACCTTCTATAGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 904 AAGAAATCAGACCTTCTATAGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 963
QY 781 AAGTGTAGTGGAGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 964 AAGTGTAGTGGAGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1023
QY 841 TGCTTGGCTGTAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
DB 1024 TGCTTGGCTGTAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1083
QY 901 TACCGCAAAAGCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
DB 1084 TACCGCAAAAGCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1143
QY 961 TCTGCGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1014
DB 1144 TCTGCGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1197

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RESULT 2
 US-09-013-634-3
 ; Sequence 3, Application US/09013634
 ; Patent No. 5945307

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; GENERAL INFORMATION:
; APPLICANT: M. Alexandra Gluckemman and Keith Robison
; TITLE OF INVENTION: LIGAND RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,634
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Attorney, Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1011
; US-09-013-634-3
;
Query Match 99.7%; Score 1006.2; DB 2; Length 1011;
Best Local Similarity 99.7%; Pred. No. 1.1e-204;
Matches 1008; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY	421	GGCGTCGACCTGTCGCTGGGCTCGGGCTTCACACACTGTGAAGCCTCGTGCAGACGTGTGACG	480
Db	421	GGGCTTGCCCTGTCTCTGGCTCGGGCTTCACACACTGTGAAGCCTCGTGTGCAGACGTGTGACG	480
OY	481	CGGCGGCGACGACGAGCGCCCTGCGCTTCGCGCGCTTTCACGTGACGCTTTCACGCTTCAGC	540
Db	481	CGGCGGCGCGGACGAGCGCCCTGCGCTTCGCGCGCTTTCACGTGACGCTTTCACGCTTCAGC	540
OY	541	TTCCGTGCTCTCTTTCGTGCTGTGCTCTGTGACGTACTCAAGGTGCTCAAGGTGTGCCCCG	600
Db	541	TTCCGTGCTCTCTTTCGTGCTGTGCTCTGTGACGTACTCAAGGTGCTCAAGGTGTGCCCCG	600
OY	601	TTCCATTGCAAGGCGATCGACGCGTATCACCATTGACAGCGGTGAGTGCCTGTGTGAGCTG	660
Db	601	TTCCATTGCAAGGCGATCGACGCGTATCACCATTGACAGCGGTGAGTGCCTGTGTGAGCTG	660
OY	661	CACCCCACTGTGTCGGGAAAGCTGTCTTGAGAGAGACAGAGCGAGCGACAGCGACCCACC	720
Db	661	CACCCCACTGTGTCGGGAAAGCTGTCTTGAGAGAGACAGAGCGAGCGACAGCGACCCACC	720
OY	721	AAGAAAGATCAGACCTTTCATAGGGAACCTTCTTGTGTGCTTGGCGCCCTATATGTGATCAC	780
Db	721	AAGAAAGATCAGACCTTTCATAGGGAACCTTCTTGTGTGCTTGGCGCCCTATATGTGATCAC	780
OY	781	AGGCTAGTGGAACTCTTTCACAGGGGCCCATGCGGCTCCCATGCGGGGGGTGTGTCCAG	840
Db	781	AGGCTAGTGGAACTCTTTCACAGGGGCCCATGCGGCTCCCATGCGGGGGGTGTGTCCAG	840
OY	841	TGCTTTGGCGTACAGCAGAGGCCCATTCGAAACCCTTTGTGTATCTTATCTGCACACACAG	900
Db	841	TGCTTTGGCGTACAGCAGAGGCCCATTCGAAACCCTTTGTGTATCTTATCTGCACACACAG	900
OY	901	TACCGCAAAAGCTGCAGAGGATTTCTGAAACAGGCTCCTGACAGACGCTTCATCTCACTCC	960
Db	901	TACCGCAAAAGCTGCAGAGGATTTCTGAAACAGGCTCCTGACAGACGCTTCATCTCACTCC	960
OY	961	TCTGGGCTTCACAGGGGACTCTCAGACGCGAAGAACTTCTGCGGTGTCTGAG	1011
Db	961	TCTGGGCTTCACAGGGGACTCTCAGACGCGAAGAACTTCTGCGGTGTCTGAG	1011

RESULT 3
 US-08-540-6508-6
 Sequence 6, Application US/08540650B
 Patent No. 6399325
 GENERAL INFORMATION:
 APPLICANT: HINUMA, Shuji
 APPLICANT: FUJII, Ryo
 APPLICANT: FUKUSUMI, Shoji
 APPLICANT: OHTAKI, Tetuya
 APPLICANT: HOSOTA, Masaki
 APPLICANT: OHGI, Kazuhiro
 APPLICANT: ONDA, Haruo
 TITLE OF INVENTION: GALANIN RECEPTOR PROTEIN, PRODUCTION AND USE THEREOF
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: US
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/540,650B
 FILING DATE: 11-OCT-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

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1      APPLICATION NUMBER: 7-134412
2      FILING DATE: 31-MAY-1995
3      APPLICATION NUMBER: 6-326610
4      FILING DATE: 28-DEC-1994
5      APPLICATION NUMBER: 6-247599
6      FILING DATE: 13-OCT-1994
7      ATTORNEY/AGENT INFORMATION:
8      NAME: RESNICK, DAVID S
9      REGISTRATION NUMBER: 34,235
10     REFERENCE/DOCKET NUMBER: 45901
11     TELECOMMUNICATION INFORMATION:
12     TELEPHONE: 617-523-3400
13     TELEFAX: 617-523-6440
14
15     INFORMATION FOR SEQ ID NO: 6:
16     SEQUENCE CHARACTERISTICS:
17         LENGTH: 1047
18         TYPE: Nucleic acid
19         STRANDEDNESS: Double
20         TOPOLOGY: Linear
21     MOLECULE TYPE: CDNA
22     FEATURE:
23     IDENTIFICATION METHOD: S
24
25     US-08-540-650B-6

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Query Match	7.8%;	Score 79;	DB 3;	Length 1047;
Best Local Similarity	49.3%;	Pred. No. 9.5e-08;		
Matches 264;	Conservative	0;	Mismatches 265;	Indels 6;
				Gaps 2

Qy 59 TGTGTGTCAAAGCGGTGGTGTGTGTGCTGTGCGTGGTGCACAGC---GGGAGCATTCGCGCG
Db 143 TGTGTGGGCAACAGCCTTAGTATTCACCTGTGCGCGCGCAGCAAGCCGGGCAAGCCGCGG
Qy 116 AGGCGCGGCGGCTTTCACCTTGACCTCAAGTGGGGAACTGTGTGTGCACCTGTGTCT
Db 203 GCACCAACCAACTGTTCATCTTCAACTGTAGAGCAATCGCGGACCTGAGCTTCTTCTTCT
Qy 176 ACATGCGCGTCAAGCTGTGGCGGGCGGTGTGGGCGAGCGGACCGGGGGGAGACCGGCTAT
Db 263 GCATTCCTTTCAGGCGCACCGTGTACCGGCTGCGCCACCTGGGTGTCTGGGCGGCTTTCAT
Qy 236 GCGCGCTGGCTGCCTTTCCTTGACACTTTCGTGGCTGGCACTTCATGCTCAGACATGGCC
Db 323 GCMAATTCATCCACTACTTCTTTCACCGTGTGCATGTGGTGGAGCATCTTCACTTCGGCC
Qy 296 CGGTACAGATTCGACCGGTGGTGGCGGTGTCTTCCCGTGAAGCTACCGGGCCAAATGT
Db 383 CCAATGTCGTGTGACCGGTACGTGTGCATCGTGCACCTGGCGGCGCTCTCTCTTCAGAG
Qy 356 GCCTCCGACAGCGGCGGCTCATGTGTGGCTTACAGTGTGTCAGCGGCTCACTTCCCA
Db 443 TGTCTCCGGAAGCGGTGTGTGGGCGTGGAGCTGCATCTGGGGGTGTTCATTGGCAI---G
Qy 416 CCGCGCGGCTGCCTGTGTCTGTGCTGGGCTTTCACAGCTGTACGGCTGTGSCACGCTGT
Db 500 CCTGTGCGGTGGCTTACACACAGGGGCTCTTTCACCGCGCGCCAGCAACAGACCTTTC
Qy 476 GGAGCGGCGGCGACAGACGAGCGCTGGGCTTCGCGCTTCACTAGGCGGCTTTCAGCGCT
Db 560 GCTGGGAGAGTGGCGCGGACCTTCGCCAAGAAAGGCTTACGTGTGTGTGSCACTTTCGTCT
Qy 536 TCAAGTCTCTGTCTCTCTTCTGTGTGTGTCTGTGTGCACGTACCTCAAGAGTGTCAA 590
Db 620 TCGGCTACTCGTGTGCGGCTCTGTGTCAATCGCTTGTGTGTGTGCAAGAGTCTTAA 674

RESULT 4
 US-09-826-509-502
 ; Sequence 502, Application US/09826506
 ; Patent No. 6806054
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Bruinsma, Karin
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin

RESULT 6
US-08-513-974B-31
Sequence 31, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:

LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-31
Query Match 7.8%; Score 79; DB 3; Length 1110;
Best Local Similarity 51.1%; Pred. No. 9.6e-08;
Matches 212; Conservative 0; Mismatches 200; Indels 3; Gaps 1;
QY 18 GGGCTTGGCGGGCTACTGTGGGACGATGGCGCTTGGCTGTCTCAACGGGCTGT 77
Db 180 GGGCTGTATGTCTGTCTGTCAACGCTGTGGTGTGGGCTGTGGGCTGTGGGCT 239
QY 78 GCTGCTTGGCTGTGTGACGAGCGCGGACATCGCGCGGCGGCGGCTGTCTTACCT 137
Db 240 GCTGTGTGTGTATCCGCGGCTGTGCGCGGCTGTGACACAGCTTCTTCTATCG 299
QY 138 GAACCTCAGTGGCGGAACTGTGTGACCGTGTCTCATGCGCTCAGCGTGGCGG 197
Db 300 CAACCTGCGCTTGTTCGAGAGTGTCTCATGTGACCGCGCTGTGCGCTCAGCGCT 359
QY 198 GCTGTGGCGGAGCGGAGCGCGG--GGGACCGCTTGTGCGCTGTGCTTCTT 254
Db 360 TGCTTTCGAGCCAGCGGCGGTGGTGTGGCGCGGCGCTGTGCGCTTCTTCTT 419
QY 255 CGACACCTTCTGTGCTGCACTCAATGCTCAGATGGCGCGGCTGACATGACGCGCTG 314
Db 420 GCAAGCGGTACCGTCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 479
QY 315 GGTGGCGGTGTCTTCCGCTGTGAGCTACCGGCGCAAGATGGCTTCCGCGCGGCT 374
Db 480 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 539
QY 375 CATGTGGCTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 429
Db 540 GCTGGCGATGTGGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTG 594
RESULT 7
US-08-776-971-26
Sequence 26, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Habata, Yugo
APPLICANT: Kawamata, Yuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Fukusumi, Shoji
APPLICANT: Kitada, Chieko
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996

FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 322:
SEQUENCE CHARACTERISTICS:
LENGTH: 1331 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 118..1227
US-08-513-974B-322

Query Match 7.8%; Score 79; DB 3; Length 1331;
Best Local Similarity 51.1%; Pred. No. 9.9e-08;
Matches 212; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

18 GGGGCTGAGCGGCTACTGCTGAGGACGATGGGCGCTCTCGCTGCTCAACGCGCTGCT 77
297 GGGGCTGATGCTGCTGCTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 356
78 GCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 137
357 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
138 GAACCTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 197
417 CAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
198 CGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
477 TGCTTGAAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
255 CGAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
537 GCACACCGTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 596
315 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 374
597 CGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
375 CATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429

Db 657 GCTGGCATTGAGCGCTCTCCGCGGTCTGCGCGCTGCTGCGCGCGCGCGCTGACACC 711

RESULT 11
US-08-776-971-103
Sequence 103, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fuji, Ryo
Fukusumi, Shoji
Kikada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 1331 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 118..1227
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-08-776-971-103

Query Match 7.8%; Score 79; DB 3; Length 1331;
Best Local Similarity 51.1%; Pred. No. 9.9e-08;
Matches 212; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

18 GGGGCTGAGCGGCTACTGCTGAGGACGATGGGCGCTCTCGCTGCTCAACGCGCTGCT 77
297 GGGGCTGATGCTGCTGCTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 356

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